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us-09-019-348-8.rspt

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 PECGKSFSQIYS----LNSHRKVHTGERP----YECGECGKSFSQRSNLMQHRRVHTG 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 9359976.

BECKER K.G., NAGLE J.W., CANNING R.D., BIDDISON W.E., OZATO K., BECKER K.G., NAGLE J.W., CANNING R.D., BIDDISON W.E., OZATO K., BECW P.D., Rapid isolation and characterization of 118 novel C2H2-type zinc finger cDNAs expressed in human brain.";
Hum. Mol. Genet. 4:689-691(1995).

EMBL; U38904; AAA93261.1 - MGD; MGI:109616; C2H2-25.

MGD; MGI:109616; C2H2-25.

PRAM; PF00096; Zf-C2H2: 11.

PROSTIE: PS00028; ZINC_FINER_C2H2; 11.

Zinc-finger; Metal-binding: DNA-binding.

Zinc-finger; AR-2154 MW; BEB9B185 CRC32;
                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CZH2 TYPE 2INC FINGER PROTEIN 25 (ZINC FINGER PROTEIN C2H2-25).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
2INC FINGER PROTEIN (FRAGMENT).
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25.5%; Score 287; DB 4; L
Best-Kocal Similarity 39.3%; Pred. No. 1.2e-20;
Matches 55; Conservative 26; Mismatches 49;
                                                              367 AA.
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ECSKCGKSFKQSSSFSSHRK 248
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                                                           PRELIMINARY;
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66 NVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALT 125
                                                                                                                                       332 SNLQTHQRVHTGEKPYTCHECGKSFNQSSHLYAHLPIHTGEKPYRCDSCGKGFSRSTDLN 391
                                                            --VSFDSSRPT----SGKMN--CDVCGLSCISF 65
                               23;
    DB 4; Length 506;
                               53; Indels
 25.4%; Score 286.5; DB 4 36.5%; Pred. No. 1.9e-20; ive 23; Mismatches 53
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Best Local Similarity 36.55
Matches 57; Conservative
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Best Local Similarity 30.4%
Matches 62; Conservative
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Best Local Similarity
Matches 56; Conserva
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SEQUENCE FROM N.A.
MEDLINE; 98074810.
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                 385 LKKHQRIHTGEKP----YKCEECGRSFNHYSILGQHQRIHTGEKPYKCKQCGKSFTQCSS 440
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                                                                                                                                                                                                                                                            WEISSIG H., MILLAN J.L.;
"A family of zinc finger genes is differentially expressed during
spermatogenesis.";
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                                                                                                                                                                                                                        Mammalia;
Mus.
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Mus.
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                                                                                                                                                                                                                                                                                                                                                                                            54; Indels
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PROSITE, PS00028; ZINC_FINGER_C2H2; 12.
Zinc-finger; Metal-binding; DNA-binding.
SEQUENCE 819 AA; 93785 MW; 011C2999 CRC32;
                                                            156 K------ERC-RTFLQSTDPGDTASAEARHIKAEMGSERAL 189
                                                                        : |: :| | | | | 501 QRIHIGEKPYKCEECGRAF-----NCRSSFIKHIR-EFIQERNL 538
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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37.5%; Pred. No. 1.8e-20;
tive 27; Mismatches 54;
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                                                                                                                                                           Created)
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BLOTTIERE L., GOUBIN G.J.;
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                                                                                                                                                                                                           Mus musculus (Mouse).
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GOUBIM G.J.;
Submitted (MAR-1998)
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092005;
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"Isolation, chromosomal localization and expression of mouse homologs of OZF, a gene encoding a zinc finger protein amplified and overexpressed in human pancreatic carcinomas.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ24763; CAB38320.1; -...CINGER_C212; 10.
Zinc-finger; Metal-binding.
DNA-binding.
SEQUENCE 292 AA; 33093 MW; OE4C7128 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                    100 IKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERC 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MURAI K., MURAKAMI H., NAGATA S.;
"A novel form of the myeloid-specific zinc finger protein (MZF-2).";
Genes Cells 2:581-591(1997).
EMBL; AB007407; BAA25190.1; -.
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Mus.
                                                                                                                                                                                                                                                          25.7%; Score 289; DB 11; Length 292; 30.4%; Pred. No. 6e-21; ive 45; Mismatches 67; Indels 3
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MYELOID ZINC FINGER PROTEIN-2.
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PROSITE; PS00028; zINC_FINGER_C2H2; 13.
PROSITE; PS00028; zINC_FINGER_C2H2; 13.
SEQUENCE 814 AA; 91667 WW; 1FC8FFCF CRC32;
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790 ACQDCGRRFNQSTKLIQHQ 808
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[1]
SEQUENCE FROM N.A.
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                                         ISSUE-OVARY;
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P70590
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STRAIN-CBA/CA CBA/C57BL, C57BL/6; TISSUE-BRAIN;
MEDLINE; 90301500
NELKI D., DUDLEY K., CUNNINGHAM P., AKHANAN M.;
-(1,0n) and sequencing of a zinc finger cDNA expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene, is expressed in
                                                                                                                                                 SECUENCE FROM N.A.
STRAINCBA/CA. CBA/C57BL, C57BL/6; TISSUE-BRAIN;
STRAINCBA/CA. CBA/C57BL, C57BL/6; TISSUE-BRAIN;
SECURINE; 96361401.
MAZARAKIS N., MICHALOVICH D., KARIS A., GROSVELD F., GALJART N.
"Zfp-37 is a member of the KRAB zinc finger gene family and is expressed in neurons of the developing and adult CNS."; Genomics 33:247-257(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                             Mammalia;
Mus.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 CKECGKSFRYN-----SSLTEHVRTHTG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 -KERCRTFLQSTDPGDTASAEARHIKAEMG 184
                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 18:3655-3655(1990).
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01-NOV-1996 (TrEMBLrel. 01, 01-MAY-1999 (TrEMBLrel. 10, ZINC-FINGER PROTEIN ZFP-37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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Q15776;
Q1-NOV-1996 (
01-NOV-1996
01-MAY-1999
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Q15776
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SETTHER REPAREMENT OF THE SET OF THE S
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EMBL; 067082; AAC61661.1; -
PFAM; PF010352; RRAB; J.
PFAM; PF00096; zf-C2H2; 7.
PROSITE; PS000298; zINC_FINGER_C2H2; 6.
Zinc-finger; Metal-binding; DNA-binding.
SEQUENCE 591 AA; 68328 MW; 047D7E62 CRC32;
                                                                                                                                                                                                                                                                                       LEE P.L., GELBART T., WEST C., ADAMS M., BLACKSTONE R., BEUTLER 1"Three genes encoding tinc finger proteins on human chromosome 6p21.3: members of a new subclass of the Kruppel gene family containing the conserved SCAN box domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.8%; Score 291; DB 11; Length 591; Best Local Similarity 37.3%; Pred. No. 8.1e-21; Matches 62; Conservative 28; Mismatches 52; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                             Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 25.9%; Score 291.5; DB 4; Best Local Similarity 40.3%; Pred. No. 7e-21; Matches 56; Conservative 24; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 43:191-201(1997).

EMBL, U57796; AAB02260.1; --

EMBL, U88079; AAC51656.1; --

EMBL, U88079; AAC51656.1; --

PFAM: PF00096; zf-C2H2; 9

PROSITE; PS00028; zIRC_FINGER_C2H2; 9.

SING-finger; Metal-binding; DNR-binding.

SEQUENCE 578 AA; 65757 MW; C0A9AD2B CRC32;
         W., LEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   591 AA.
BEUTLER E., GELBART T., WEST C., KUHL W
Blood Cells Mol. Dis. 21:206-216(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRAB-ZINC FINGER PROTEIN KZF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 KCEFCGRSYKQRSSLEEHK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    547 QCNECGKAFIQRSSLIRHQ 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, 01-JUN-1998 (TrEMBLrel. 06, 01-MAX-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                                     [3]
SEQUENCE FROM N.A.
MEDLINE; 97386587.
                                                                                     SEQUENCE FROM N.A.
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162 FLQS------TDPGDTASAEARHIKAEMG---SERALVLDRLASNVAKRKSSMP 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 LHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRT 161
                                                                                                                                                                                                                                               16 EEPEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCGLSCISFNVLMVHKRSH 75
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                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 346;
                                                                                        Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 PYECNECGKAFSQHSSLQQHK-RTHTGEIPYECNECGKAFSQHSSLQM 220
                                                                                                                                                      27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.5%; Score 298.5; DB 11; Length Best Local Similarity 35.1%; Pred. No. 8.3e-22; Matches 59; Conservative 34; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Studies on zinc-finger protein genes expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=ICR; TISSUE=TESTIS; FUJIWARA Y.; Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 PYKCEFCGRSYKQRSSLEEHKERCRTFLQSTDPGDTASAEARHIKAEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
ZINC FINGER PROTEIN (FRAGMENT).
                                                                                        Score 347.5; DB 1
Pred. No. 1.2e-26;
CCC9E71E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER 1 1 SEQUENCE 346 AA; 39665 MW; 06C78AAD CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 AA.
                                                                                 Query Match 30.9%; Score 347.3;
Best Local Similarity 55.3%; Pred. No. 1.2e
Matches 68; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               594
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Thesis (1991), Unknown Institution.
EMBL; DIO627; BAAO1477.1;
PFAM: PFO0096; zf-c2H2: 12.
PROSITE; PSO0028; ZINC_FINGER_C2H2; 12.
Zinc_finger; Metal-binding; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q62514 PRELIMINARY; PRT;
Q62514;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
37116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUJIWARA Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 QKF 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORF 123
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       962512
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Q62514
ID Q62514
AC Q62514
DT 01-NOV
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Q62512
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                                                                              MEDLINE; 98056818.
HANSEN J.D., STRASSBURGER P., DU PASQUIER L.;
HANSEN J.D., STRASSBURGER P., DU PASQUIER L.;
"Conservation of a master hematopoietic switch gene during vertebrate evolution: isolation and characterization of Ikaros from teleost and amphibian species.";
Eur. J. Immunol. 27:3049-3058(1997).
-! FUNCTION: BINDS AND ACTIVATES THE ENHANCER
(DELTA-A ELEMBRY) OF THE CD3-DELTA GENE.
FUNCTIONS IN THE SPECIFICATION AND THE MATURATION OF THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 YKCEFCGRSYKQRSSLEEHKERCRTFLQSTDPGDTASAEARHIKAEM-----GSERAL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 GERPFQCNQCGASFTQKGNLLRHIKLHTGERPFKCHLCNYACQRRDALTGHLRTHSVEKP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                      ALSO INTERACTS WITH A CRITICAL CONTROL ELEMENT IN THE TDT
(TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) PROMOTER AS WELL AS WITH
THE PROMOTERS FOO OTHER GENES EXPRESSED DURING EARLY STAGES OF B
AND T CELL DEVELOPMENT.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SUBCELLULAR LOCATION: NUCLEAR.
NO EXPRESSION IN MOSCLE.
-!- SIMILARITY: TO D. MELANOGASTER HUNCHBACK.
EMBL; U92202; AAB53435.1;
-- SIMILARITY: TO D. MELANOGASTER HUNCHBACK.
PROSITE; PSO0028; ZINC. FINGER. C2H2; 3.
PPRAM: PF00096; zf-C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Amphibia:
Batrachia: Anura; Mesobatrachia; Pipoidea; Pipidae: Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation; Activator; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein.

NON_TER 1 1 1 1 1 1 1 2N_FING 5 27 C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
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Pred. No. 9.8e-47;
9; Mismatches 18; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
IKAROS-RELATED TRANSCRIPTION FACTOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW; 2B786CAD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

TURPEN J., KELLEY C., MEAD P., ZON L.;
Immunity 0:0-0(1997).

EMBL; AF02449; AAB81280.1; -.

PFAM; PF00096; zf-C212; 2.

PROSITE; PS00028; ZINC_FINGER_C212; 2.

Zinc_finger; Metal-binding; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.6%; Sccilarity 75.4%; Pre
Conservative 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 VLDRLASNVAKRKSSMPQ 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33
61
138
138 AA;
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Best Local Similarity
Matches 104; Conserv
                                                        FROM N.A.
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Mismatches

417 AA

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68 DKDDSVIVEDSLSEPLGYCDGSGPEPHSP--------GGIRLPNGK 105
                                                                                                                                                                                                       113 LCNYACQRRDALTGHLRTHSVE-----KPYKCEFCGRSYKQRSSLEEHKERCRTFLQ--S 165
                                                              1 ERDENVL----KSEPM----GNAEEPEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Sakaryota: Metazoa: Chordata: Craniata: Vertebrata: Actinopterygii;
Neopterygii: Teleostei: Euteleostei: Acanthopterygii: Percomorpha:
Tetraodontiformes; Tetraodontoidei: Tetraodontidae; Fugu.
                                                                                                                                                                                                                                                                          166 TD-----PGDTASAEARHIK-----AEMGSERALVLDRLASNVAKRKSSMPQKF 209
                                                                                                                                                                                                                                                                                              GELLURE K., BRENNER S.;
GELLURE K., BRENNER S.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF056116; AAC3487.1; -.
PFAM; PF00096; zf-C2H2; 5.
PROSITE; PS00028; zINC-FINGER_C2H2; 5.
Zinc-finger: Metal-binding; DNA-binding.
SEQUENCE 417 AA; 45664 MW; 7856E12F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
53.6%; Pic. 23;
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                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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              Similarity
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          Local Simi
hes 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKAROS-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 KGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 EEHKERCRTFLQS-----TDPGDTASAEARHIKAEM-GSERALVLDRLASNVAKRKS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 EEHKERCHNYLQCMGLQNSIYIVKEENSQNEQRE---DMPASERALVLDRIANNVAKRKS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    43
                                          Brachydanio rerio (Zebrafish) (Zebra danio).
Subkaryota: Metazoa: Chordata: Craniata: Vertebrata; Actinopterygii;
Neopterygii: Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea: Cyprinidae: Rasborinee; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMMA Y., KIYOSAWA H., MORI T., OGURI A., NIKAIDO T., KANAZAWA K., TOJO M., TAKEDA J., TANNO Y., YOKOYA S., KAWABATA I., IKEDA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PYSYSREYNEYENIKLERHVVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 DSSRPTSGKMNCDVCGLSCISFNVLMVHKRSHT-------GERPFQCNQCGASFTQ
                                                                                                                                                                                                                                                                                                                                                                                                 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
Mus.
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                                                                                                                                                                                                                                                                                                                                                                Length 537;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Eos: a novel member of the Ikaros gene family expressed predominantly in the developing nervous system.";
PEBS Lett. 0:0-0(1999).
PEMBL; AB017615; BA3436131;
PROSITE: PS00028 ZINC_FINGER_C2H2; 5.
Zinc-finger; Metal-binding; DNA-binding.
SEQUENCE 533 AA; 58167 MM; 2A0315AD CRC32;
                                                                                                                                                              AMEMIYA C., KAWASAKI H.; "Characterization of zebrafish ikaros, a gene necessary
                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
         01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                            57.7%; Score 650; DB 13; 55.7%; Pred. No. 3.5e-56; ative 17; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.7'
Matches 137; Conservative
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                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                   TISSUE-SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ICR;
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RESULT

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                                                                                            112 RLPNGKLQCEICGIVCTGPNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHSGE 171
                                                                                                                                             107 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA-BINDING PROTEIN IKAROS (LYMPHOID TRANSCRIPTION FACTOR LYF-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis/gilli.
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                     ÷,
   DB 13; Length 417;
                                     Indels
                                                                                                                                                                                                                    167 DPGDTASAEARHIKAE---MGSERALVLDRLASNVAKRKSSMPQKF 209
                                                                                                                                                                                                                                       35;
51.4%; Score 578.5; DB 1
62.0%; Pred. No. 2.9e-49;
tive 25; Mismatches 35
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

	Seconds
	24.57
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	Search
	••
sw model	08:05:41
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Title: US-0

BLOSUM62 Scoring table:

201082 seqs, 61543640 residues Database : Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O08900 mns mascala			P79751 fugu rubrip	0	xenopus			Q15776 homo sapien		Q9z1d8 mus musculu	snw	O70162 mus musculu	homo	рошо	ОШО	ratt	043345 homo sapien	ОШО	Q14586 homo sapien	homo	homod		homo	Q02313 homo sapien	000455 homo sapien	homo	095779 homo sapien	homo
	ID	008800	1 093581	1 092222	3 P79751	3 013100	3 042244	062512	1 062514	Q15776	P70590	1 Q9Z1D8	500260 1	070162	Q13398	014898	060765	062886	043345	075802	014586	043693	095015	. 035483	043724 .	002313	000455	060792	095779	095780
	DB	11	13	11	13	13	13	11	11	4	11	11	11	11	4	4	4	11	4	4	4	4	4	11	4	4	4	4	. 7	4
	Query Match Length DB	507	537	533	417	138	328	346	594	578	591	819	292	814	367	206	605	650	1167	612	732	395	430	812	1207	427	382	751	445	498
æ	Query	91.0	57.7	54.8	51.4	48.6	30.9	26.5	26.2	25.9	25.8	25.7	25.7	25.6	25.5	25.4	25.4	25.4	25.3	25.3	25.2	25.2	25.2	25.2	25.2	٠.	24.9	24.8	24.8	24.8
	Score	1024.5	650	617	578.5	547.5	347.5	298.5	295	291.5	291	289	289	288	287	286.5	286	286	285	284.5	284	284	284	284	283.5	281.5	280	279.5	279	279
	Result No.	П	7	m	4	S	9	7	œ	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29

014709 homo sapien Q14593 homo sapien	092251 homo sapien 043167 homo sapien 043309 homo sapien 014588 homo sapien	Q62517 mus musculu O43296 homo sapien Q61491 mus musculu	Q9z2x6 mus musculu Q15917 homo sapien Q09046 xenopus lae	092269 homo sapien 043387 homo sapien 014978 homo sapien 075260 homo sapien
014709	092951 043167 043309 014588	Q62517 Q43296 Q61491	Q9Z2X6 Q15917 Q09046	Q92969 O43387 O14978 O75260
44	444	141	11 13	4 4 4 4
1029	273 697 604 693	184 627 546	587 622 591	151 683 683 393
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24	7 7 7 7	24 24 24 24	24 24 24 24	24.3 24.2 24.2 2.2 2.2
278	27.5 27.5 77.5 77.2	277 276.5 276.5	276.5 276 275	273.5 273 273 273
30	3 3 3 3 2 4 3 5	36 37 38	39 4 4 1.	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                   56 DVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCN 115
                                                                                                                                                                                                                                                                                                                                            : || : | | | || || || || || EECGRAFNRHKRIHJGEKPYRCEECG 317
                                                                                                                                                                                                                                                                      102 EECGKAFKWSLIFNEHKRIHTGEKPFTCEECGSIFTTSSHFAKHKIIHTGEKP----YKC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FERBUS D., LE CHALONY C., PROSPERI M.-T., MULERIS M.,
VINCENT-SALOMON A., GOUBIN G.;
"Identification, nuclear localization, and binding activities of .OZF,
a human protein solely composed of zinc-finger motifs.";
EUR. J. BIOCHEM. 236:991-995(1996).
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: LIVER, SKELETAL AND HEART MUSCLE, MAMMARY
CELLS. VERY LOW LEVELS IN BRAIN, LUNG, PLACENTA, AND KIDNEY.
-!- SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                           16 EEPEIPYSYSREYNEYENI-------KLERHVVSFDSSRPTSGKMNC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 94149744.
LE CHALONY C., PROSPERI M.-T., HALUZA R., APIOU F., DUTRILLAUX B.,
                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                    Length 474;
                                                                                                                                                                    ; DB 1; Length 474
8.9e-19;
ches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     318 KAFNRSTTLTKHKRIHTGEKPYTCEECGKAFRQSSKLNEHKK 359
                                                                                                                                                                                                                                                                                                                                                                                            116 YACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKE 157
 C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
C3H2-TYPE.
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 AA
                                                                                                                                                                                     ; Pred. No. 8.9e
22; Mismatches
                                                                                                                                                                  Ouery Match 25.7%; Score 289; Best Local Similarity 34.6%; Pred. No. 8 Matches 56; Conservative 22; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 601505; -
PROSITE; PS00028; ZINC_FINGER_C2H2; 10.
PFAM; PF00096; zf-C2H2; 10.
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                                                                                                                 MM;
333
361
389
417
445
473
55249 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPIENS (HUMAN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q15072;
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SEQUENCE
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OZF_HUMAN
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100 IKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 ENLLTHOKIHTGEKPFECKDCGKAFIQKSN--LIRHORTHTGEKPFVCKECGKTFSGKSN 142
                                                                                                                                                                                                                                                                                                 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                            --------CDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRH 99
                                                                                                                                                                                                                                                                                                                              ENVLKSEPMGNAEEPEIPYSYSREYNEYENIKLERHVVSFDSSRP-----TSGKMN 54
                                METAL-BINDING; NUCLEAR PROTEIN; REPEAT
                                                                                                                                                                                                                                                               Length 292;
                                                                                                                                                                                                                                                                                                 68; Indels
                                                                                                                                                                                                                                                               25.6%; Score 288; DB 1;
30.4%; Pred. No. 6.5e-19;
tive 44; Mismatches 68
                                                                                                                                                                                                                   786C268C CRC32;
                                             ZINC-FINGERS.
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 RTF---LQSTDPGDTASAEARHIK 180
                                                                                                                                                                                                                    33280 MW;
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.4%.
Matches 62; Conservative
                                  ZINC-FINGER; DNA-BINDING;
                                                292
388
94
1122
206
234
292
HSSP; P25490; 1ZNM.
FRANSFAC; T02323; -
                                                                                                                                                                                  ZN_FING
ZN_FING
SEQUENCE
                 RANSFAC
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Search completed: November 6, 1999, 11:46:21 Job time: 6525 sec

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                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                       165 FSQSMNLTVHQRTHTGEKPYQCKECGKAFRKNSSLIQHERIHTGEKPYKCHDCGKAFSKN 224
                                                                                                                             62 CISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRR 121
                                                                                                               2 RDENVLKSEPMGNAEEPEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCGLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR PROTEIN; REPEAT
                                                                                            .
9
                                                                                                                                                                                                                                                                                                                                                                 ROS TAURUS (BOVINE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACIYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE;
                                                                     Length 347;
                                                                  Score 290; DB 1;
Pred. No. 5.2e-19;
4; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC32;
         C2H2-TYPE.
C2H2-TYPE.
F042FE59 CRC32;
                                                                                                                                                                                                                                                                                                Q28151;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ZINC FINGER PROTEIN OZF.
                                                                                                                                                                                                                     SSLTQHRRIHTGEKPYECMICGKHFTGRSSLTVHQ 259
                                                                                                                                                                                                        122 DALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHK 156
                                                                                                                                                                                                                                                                                       292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21NC-FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-BINDING; METAL-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88B8A3DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X81804; E213761; ALT_INIT.
PROSITE; PS00028; ZINC_FINGER_CZH2; 10.
PFAM: PF00096; Zf-CZH2; 10.
HSSP: P25490; 12NM.
                                                                                                                                                                                                                                                                                       PRT;
                                                                                          34;
                                   39855 MW;
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                                                                   25.8%;
34.8%;
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                                                                                           Conservative
                                                                                                                                                                                                                                                                                       STANDARD;
 268
296
324
347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC-FINGER;
                                                                                          54;
                                                                                                                                                                                                                                                                                       OZF_BOVIN
ZN_FING
ZN_FING
ZN_FING
SEQUENCE
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ZN_FING
ZN_FING
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ZN_FING
SEQUENCE
                                                                   Query Match
Best Local
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ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                 RESULT 13
OZF_BOVIN
                                                                                          Matches
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TOWNERUP N., AAGAARD L., LUND C.L., BOEL E., BAXENDALE S., BATES G.P.,
TEHRACH H., VISSING H.;
LEHRACH H., VISSING H.;
A Zinc-finger gene ZNF141 mapping at 4p16.3/D4S90 is a candidate
gene for the Wolf-Hirschhorn (4p-) syndrome.";
HUM. MOL GENET. 2:15771-1575(1993).
-!- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION AS A
REPRESSOR. CANDIDATE GENE FOR WOLF-HIRSCHHORN (4P-) SYNDROME
                                                                                                      85 ENLLTHOKIHTGEKPFECKDCGKAFIQKSN--LIRHQRTHTGEKPFICKECGKTFSGKSN 142
                                                                                                                                                              100 IKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERC 159
                                                                                                                                                                                                                              203 VRIHSGDKPYECNVCGRAFSQSSSLTVHVRSHTGEKPYGCNECGRAFSQFSTLALHL-RI 261
                                     Gaps
                                                                      4 ENVLKSEPMGNAEEPEIPYSYSREYNEYENIKLERHVVSFDSSRP-----TSGKMN 54
                                                                                                                                          ------CDVCGLSCISENVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRH 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- TISSUE SPECIFICITY: UBIQUITOUSLY LOW EXPRESSION.
-i- SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPRESSOR; ZINC-FINGER; METAL-BINDING;
                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 Length 292;
                                     67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOX").
 Score 289; DB 1;
Pred. No. 5.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRAB BOX ("A B KRAB BOX ("B B ZINC FINGERS. C2H2-TYPE. C2H2-TYPE. C2H2-TYPE. C2H2-TYPE.
                                   45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L15309; G347906; --
MIM; 194648; --
PROSITE; PS00028; ZINC_FINGER_C2H2; 10.
PFAM; PF00096; Zf-C2H2; 10.
HSSP; P080447; 1SP2.
TRANSCRIPTION REGULATION; REPRESSOR; ZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 KRAB BOX.
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                 160 RIF---LQSTDPGDTASAEARHIK 180
                                                                                                                                                                                                                                                                                                      262 HIGKKPYQCSECGKAFSQKSHHIR 285
25.7%;
30.4%;
                                   62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (REL. 37, LAS ZINC FINGER PROTEIN 141.
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
Ouery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-INSULINOMA;
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DOMAIN

2
DOMAIN

44
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01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                  Z141_HUMAN
Q15928;
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ZN_FING
ZN_FING
ZN_FING
ZN_FING
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                                  Matches
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13
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                                                                        PTSGK-MNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
               BRADY J.P., DUNCAN M.K., WAWROUSEK E.F., PIATIGORSKY J.;
SUBMITTED (PAR-1996) TO EMBL/GENBANKADBU DATA BANKS.
-!- FUNCTION: IT MAY PLAY A ROLE IN RENAL DEVELOPMENT AND MAY
ALSO BE INVOLVED IN THE REPAIR OF THE KIDNEY AFTER ISCHEMIA-
REPERREVISION OR FOLIC ACID ADMINISTRATION.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARIIY: BELONGS TO THE KNUEPPEL SUBFAMILY OF C242-TYPE ZINC-
-!- SIMILARIIY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L77247; G1256362; -. MGD; MGI:103172; TCF17. PROSITE; PS00028; ZINC_FINGER_C2H2; 13. PF00006; zf-C2H2; 13. PFSSP; P00047; 1SP2. ZINC_FINGER; TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVATOR;
                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                               01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
                                                      107 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN; METAL-BINDING DOMAIN 12 53 KRAB BOX ("A BOX").

DOMAIN 54 85 KRAB BOX ("B BOX").

DOMAIN 184 567 ZINC-FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4F7FBBDC CRC32;
                                                                                                                                                                                                                    572 AA
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C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                    328 CKECGKSFRYN-----SSLTEHVRTHTG 350
                                                                                                                156 -KERCRIFLQSTDPGDTASAEARHIKAEMG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2H2-TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: CONTAINS 1 KRAB BOX.
                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQ
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545
572 AA;
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LENS;
                                                                                                                                                                                                                   KID1_MOUSE
Q61751;
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SEQUENCE
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Length 572;

26.0%; Score 293; DB 1;

Query Match

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                                                                                                                                                                                                            | || | : : | : | | | | 374 EKPYRCSECGKGFTSISRLNRHRIIHTGEK----FYNCNECGKALSSHSTLIIHERIHTG 429
                                                                                                                                                          EKPCKCKVCGKAFRQSSALIQHQRMHTGERPYKCNECGKTFRCNSSLSNHQRTHTGEKPY 489
                                                                                                                                                                                           138 KCEFCGRSYKQRSSLEEHKE-----RC----RTFLQSTDPGDTASAEARHIKAEMGS 185
                                                                                                                          ERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPY 137
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHOWDHURY K., DEUTSCH U., GRUSS P.; "A multigene family encoding several 'finger' structures is present and differentially active in mammalian genomes."; CELL 48:771-778(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHOWDHURY K., DRESSLER G., DREIER G., DEUTSCH U., GRUSS P.; The primary structure of the murine multifinger gene mKr2 and its specific expression in developing and adult neurons."; EMBO J. 7:1345-1353(1988).
                                                        EIPYSYSREYNEYENI-KLERHVVSFDSSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTG
                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: CAN BE A REGULATORY FACTOR REQUIRED FOR THE DIFFERENTIATION AND/OR PHENOTYPIC MAINTENANCE OF NEURONS.
                          Indels
Pred. No. 4.8e-19;
                                                                                                                                                                                                                                                                                                                                                                        KRZ_MOUSE STANDARD; PRT; 34, AA. 108043; 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE) 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) MKRZ PROTEIN (ZINC FINGER PROTEIN 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC-FINGERS.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 75-347 FROM N.A. MEDLINE; 87131089.
     ilarity 33.7%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y00850; G52811; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G193352; -
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PIR; B26595; B26595.
MGD; MGI:99167; ZFP2
   Best Local Similarity
Matches 61; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                            186 E 186
                                                                                                                                                                                                                                                                                           543 K 543
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                                                                           01-AUG-1990 (REL. 15, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ZINC_FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC-FINGER; METAL-BINDING; DNA-BINDING; NUCLEAR PROTEIN; REPEAT; DEVELOPMENTAL PROTEIN; SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-TESTIS;
MEDLINE; 90301500.
NELKI D., DUDLEY K., CUNNINGHAM P., AKHAVAN M.;
"Cloning and sequencing of a zinc finger cDNA expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                BURKE P.S., WOLGEMUTH D.J.;
"Zifp-37, a new murine zinc finger encoding gene, is expressed developmentally regulated pattern in the male germ line.";
NUCLEIC ACIDS RES. 20:2827-2834(1992).
                                                                                                                                                                                                                                     MUS MUSCIUUS (MOUSE).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEIC ACIDS RES. 18:3655-3655(1990).
-!- FUNCTION: MAY HAVE A ROLE IN REGULATING SPERMIOGENESIS.
-!- SIMILARITY: CONTAINS 1 KRAB BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPERMATOGENESIS.,
21NC-FINGERS.
21NC-FINGERS.
C2H2-TYPE.
C2H2-TYPE
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EMBL; X52533; G53457; ALT_INIT.
PIR; S10245; S10245.
PIR; S22954; S22954.
MGD; MGI:99181; ZFP37.
PROSITE: PS000026; Z1NC_FINGER_C2H2; 11.
HSSP; P000047; 1592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 177-553 FROM N.A.
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                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92310982.
                                                                                                                                                                                     PROTEIN).
ZFP37 OR ZFP-37.
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-TESTIS
                      ZF37_MOUSE
P17141;
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CONFLICT
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ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            testis.
                              Query Match 26.3%; Score 296; DB 1; Length 1191;
Best Local Similarity 34.9%; Pred. No. 5.6e-19;
Matches 66; Conservative 29; Mismatches 78; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTH 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGNAEEPEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCGLSCISFNVLMVH 71
                                         EMBL; L11672; G186774; -.
EMBL; MG1817; G18440; ALT_SEQ.
PIR; F39384; F39384.
PIR; S35305; S33305.
PROSITE: PS00028: ZINC_FINGER_C2H2; 31.
PROSITE: P08047; 1SP2.
ZINC_FINGER; DNA-BINDING; METAL_BINDING; NUCLEAR PROTEIN; REPEAT.
                                                                                                                                                                                                                                                                                                                   C2H2-TYPE (DEGENERATE).
C2H2-TYPE (C2H2-TYPE).
                                                                                                                                                                                                                                                                   KRAB BOX ("A BOX").
KRAB BOX ("B BOX").
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4D6A45E4 CRC32;
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              988
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ETILANTVK 1187
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SEQUENCE
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Gaps 20; 26.1%; Score 294; DB 1; Length 553; 38.0%; Pred. No. 3.7e-19; 44; Indels Mismatches 29; Conservative Query Match Best Local Similarity Matches 57; Conserv

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01-JUN-1994
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                         ZN91_HUMAN
Q05481;
                                                                                                                              ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
  ZN_FING
                                                                                                                  ZN_FING
                                                                                                                                                                                                                                                                                                                                                        RESULT 9
ZN91_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     НОМО
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                                                                                               .,
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                                                                                                                                                          44 DSSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLH 103
                                                                                                                                                                                  582
                                                                                               Gaps
                                                                                                                  -----KLERHVVSF 43
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 91317761.

MEDLINE; 91317761.

HOWARA R., COLLINS S.J., HICKSTEIN D., RASKIND W., DEAVEN L.L.,
O'HARA P., HAGEN F.S., KAUSHANSKY K.;

"A retinoic acid "responsive human zinc finger gene, MZF-1,
preferentially expressed in myeloid cells.";
J. BIOL. CHEM. 266.14183-14187(1991).
I- FUNCTION: MAY BE ONE REGULATOR OF TRANSCRIPTIONAL EVENTS DURING
HEMOPOIETIC DEVELOPMENT.
I- SUBCELLULAR LOCATION: NUCLEAR.
I- SUBCELLULAR LOCATION: NUCLEAR.
I- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN DIFFERENTIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYELOID CELLS.
-!- INDUCTION: BY RETINOIC ACID.
-!- SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGULATION; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.

1 23 ACPL-TYPE ZINC-FINGERS.

14 235 GLY/PRO-RICH.

26 482 9 C242-TYPE ZINC-FINGERS.
                                                                                                                                     473 EKPYKCEECGKA----FSRSSNLTKHKKIHIEKKPYKCEECGKAFKWSSKLTEHKITH
                                                                                                                                                                     30;
                                                                                                                                                                                                                 104 TGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHK 156
                                                                                                                                                                                                                                                                                                                                                               CHORDAIA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                          Length 803;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                 01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 24, LAST ANNOTATION UPDATE)
ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).
                                                                                              26;
                                5
          C2H2-TYPE.
C2H2-TYPE.
P -> S (IN REF. 2).
7; DB052880 CRC32;
                                                                         DB 1;
                                                               Score 299; Db 1,
No. 2e-19;
                                                                  26.6%; Scole 35.3%; Pred. No. 2e-19,
                                                                                                                                                                                                                                                                              485 AA
                                                                                                                 4 ENVLKSEPMGNAEEPEIPYSYSREYNEYENI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00028; ZINC_FINGER_C2H2; 13.
PFAM; PF00096; Zf-C2H2; 13.
HSSP; P25490; 1ZNM.
                                                                                                                                                                                                                                                                                                                                                                         PRIMATES; CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                              PRT;
                                           ..
Μ
                                          93487
                                                                       Query Match
Best Local Similarity 35.37
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M58297; G189044; -.
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A40751; A40751.
MIM; 194550; -
                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
700
728
756
181
803 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSFAC; T00529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANSCRIPTION
                                                                                                                                                                                                                                                                              ZN42_HUMAN
ZN_FING
ZN_FING
ZN_FING
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                      P28698;
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                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || :| :| || :| || :| || || 351 PECGORFS-----QRLKLTRHQRTHTGEKP----YHCGECGLGFTQVSRLTEHQRIHTG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPY 137
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MARTIAL J.A.;
"The evolutionarily conserved Kruppel-associated box domain defines subfamily of eukaryotic multifingered proteins.";
PROC. NATL. ACAD. SCI. U.S.A. 88:3608-3612(1991).
-: SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-: SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 9322867.
BELLEFROID E.J., MARINE J.C., RIED T., LECOCQ P.J., RIVIERE M.,
AMEMIYA C.T., PONCELET D.A., COULIE P.G., DE JONG P.J.,
SZPIRER C., WARD D.C., MARTIAL J.A.;
Clustered organization of homologous KRAB zinc-finger genes with
enhanced expression in human T lymphoid cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                           Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UN-1994 (REL. 29, CREATED)
UN-1994 (REL. 29, LAST SEQUENCE UPDATE)
CS-1998 (REL. 37, LAST ANDTATION UPDATE)
FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BELLEFROID E.J., PONCELET D.A., LECOCO P.J., REVELANT O.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       50;
                                                                                                                                                                                                                                                                                                                                                                      Score 297; DB 1;
Pred. No. 1.8e-19;
2; Mismatches 50
                                                                                                                                                                                                                                                                                                    CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1191 AA.
                                                                                                                                                                                                                                                                                                 908B33F1
C2H2 - TYPE.
                                                                                                                                                                                                                                                C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                 MW.
                                                                                                                                                                                                                                                                                                                                                                      26.4%;
41.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 ACQDCGRRFHQSTKLIQHQ 479
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SEQUENCE OF 15-204 FROM N.A.
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 41.00,
-hos 57; Conservative
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342
398
498
454
54463 X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                 485 AA;
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Page 5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The evolutionarily conserved Kruppel-associated box domain defines subfamily of eukaryotic multifingered proteins.";
PROC. NATL. ACAD. SCI. U.S.A. 88:3608-3612(1991).
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- TISSUE SPECIFICITY: T AND B CELL LINES.
-!- SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
-!- SIMILARITY: CONTAINS 1 KRAB BOX.
                                                                                                                                                                                                                                                                                                                                                     TISSUE-T-CELL;
MEDLINE; 91279444.
LOVERING R., TROWSDALE J.;
LOVERING R., TROWSDALE J.;
Mphone encoding 22 highly related zinc fingers is expressed in lymphoid cell lines.;
NUCLEIC ACIDS RES. 19:2921-2927(1991).
                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-BINDING; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRAB BOX ("A BOX").

KRAB BOX ("B BOX").

Z C2H2-TYPE.

C2H2-TYPE.

C2H2-TYPE (DEGENERATE).

C2H2-TYPE (DEGENERATE).

C2H2-TYPE (DEGENERATE).

C2H2-TYPE.

C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91219421.
BELLEFROID E.J., PONCELET D.A., LECOCQ P.J., REVELANT
                                                                                                        01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24; LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
21-CE FINGER PROTEIN 43 (ZINC PROTEIN HTF6).
2NF43.
                                                                      803 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X59244; G38032; --
EMBL; M61869; G184450; --
PIR; S2683; S26823.
PIR; D39384; D39384,
PROSITE; PS00028; ZINC_FINGER_C2H2; 19.
PRAM: PF00096; zf-C2H2; 21.
HSSP; P25490; IZNM.
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 38-190 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC-FINGER; METAL-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
    ZN43_HUMAN
ID ZN43_HUMAN
AC P28160;
T 01-7-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                           4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 DSVVGTDPLSSQNVASSPYSCSKCRKTFKRWK-----SFLNHQQTHSREKPYLCSHCNK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFIQNSDLVKHFRTHTGERPYQCAECHKGFIQKSDLVKHLRTHTGERPFKCSHCDKKFTE 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.2%; Score 317.5; DB 1; Length 1350; 36.9%; Pred. No. 7.6e-21; ive 33; Mismatches 59; Indels 21;
                 PROSITE: PS00028; ZINC_FINGER_C2H2; 35.
PFAM; PF00096; Zf-C2H2; 36.
ZINC-FINGER; METAL-BINDING; RRA-BINDING; REPEAT; 3D-STRUCTURE;
                                                                                                                     BOX").
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1052 1052
1056 1065
1066 1066
1350 Aa; 155804 MW; 10CA7C8C CRC32;
                                                                                                                KRAB BOX ("A BOX")
ZINC-FINGERS II.
ZINC-FINGERS II.
ZINC-FINGERS III.
ZINC-FINGERS III.
ZINC-FINGERS V.
ZINC-FINGERS V.
                                                                                                                                                                                                                                                                                                      CC2H2 - TYPE

CC
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Best Local Similarity 36.9%
Matches 66; Conservative
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10010
10010
10066
11158
11242
11242
11242
11243
11243
11065
11065
11065
PDB; 12NF; 15-OCT-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1044
1136
1164
                                                                                            PHOSPHORYLATION
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ZN FIN
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                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94021366.
ANDREAZZOLI M., DE LUCCHINI S., COSTA M., BARSACCHI G.;
"RNA binding properties and evolutionary conservation of the Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: PHOSPHORYLATED. SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS LETT. 254:159-164(1989).
-!- FUNCTION: BINDS RNA.
-!- FUNCTION: BINDS RNA.
-!- SUBGELLULATION PROCESSES.
-!- SUBGELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: OCCYTES AND IN SPECIALIZED CELL TYPES SUCH
-!- RETINA COMPS.
-!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT OOGENESIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 89346749.
LEE M.S., GIPPERT G.P., SOMAN K.V., CASE D.A., WRIGHT P.E.;
"Three-dimensional solution structure of a single zinc finger DNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 89378224.
LEE M.S., CAVANAGH J., WRIGHT P.E.;
"Complete assignment of the 1H NMR spectrum of a synthetic zinc finger from Xfin. Sequential resonance assignments and secondary
                                                                                                                                                                                                                                                                                                                                                                                                                               RUIZ I ALTABA R., PERRY-O'KEEFE H., MELTON D.A.;
"Xfin: an embryonic gene encoding a multifingered protein in
                                                      ------AEMGSERALVLDRLASNVAKRKSSMPQKF 209
                                                                          DOMAIN: CONTAINS 37 FINGER MOTIFS IN 6 DOMAINS.
                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multifinger protein Xfin.";
NUCLEIC ACIDS RES. 21:4218-4225(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 KRAB BOX.
                                                                                                                                                                                                                                                                                                        XENOPUS LAEVIS (AFRICAN CLAWED FROG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF FINGER 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF A FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCIENCE 245:635-637(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 6:3065-3070(1987)
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X06021; G65234; -. PIR; S00647; S00647.
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08,
37,
                                                                                                                                                                                                                                 (REL.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 88082679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBRYOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=EMBRYO;
                                                                                                                                                                                                                                                                      XFIN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure.";
                                                                                                                                                                                                                                 01-AUG-1988
15-DEC-1998
                                                                                                                                                                           XFIN_XENLA
P08045;
                                                                                                                                                                                                                01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multifinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding
                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                PERSONANCE FROM N.A., AND SEQUENCE OF 246-267-AND 289-306.

STRAIN-BALB/C: TISSUE-THYMUS;

MEDLINE: 98180981.

A HAHM K., COBB B.S., MCCARTY A.S., BROWN K.E., KLUG C.A., LEE R.,

A RAKASHI K., WEISSMAN I.L., FISHER A.G., SMALE S.T.;

"Helios, a T cell-restricted itsaros family member that quantitatively associates with Irsaros at centromeric heterochromatin.";

"Helios, a T cell-restricted farios family member that quantitatively associates with Irsaros at Centromeric heterochromatin.";

"Helios, a Coll-restricted farios at Centromeric heterochromatin.";

"Helios, a Coll-restricted farios at Centromeric heterochromatin.";

"Helios, a T cell-restricted farios at Centromeric heterochromatin.";

"Helios, a Miles Secolates with Irsaros at Centromeric heterochromatin.";

"Helios, a Miles Secolates with Irsaros at Centromeric heterochromatin.";

"Helios, a Miles Secolates with Irsaros at Centromeric heterochromatin.";

"Helios, a Miles Secolates with Irsaros at Centromeric heterochromatin.";

"Helios, a Miles Secolates with Irsaros at Centromeric heterochromatin.";

"Helios, a Miles Secolates with Irsaros at Centromeric heterochromatin.";

"Helios, a Miles Februssian in Splesn, LIVER, KIDNEY OR MUSCLE.

"Helios, a Miles Februssian in Splesn, LIVER, FROTEIN."

"Helios, a Miles Februssian in Splesn, LIVER, FROTEIN."

"Helios, a Miles Februssian in Splesn, Miles Froteins."

"Helios, a Miles Februssian in Splesn, Miles Froteins."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RDENVLKSEPMGNAEEPEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCGLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P08047; ISP2.
TRANSCRIPTION REGULATION; ACTIVATOR; ZINC-FINGER; METAL-BINDING;
                                                                                                                                                                                                                                                               EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ROBENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                  54.9%; Score 618; DB 1; Length 526; 52.7%; Pred. No. 3.6e-48; ive 31; Mismatches 53; Indels
167 D-PG-----DTASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RR PROTEIN; ALTERNATIVE SPLICING.
219
219
210
21NC FINGERS I.
21NC FINGERS II.
34
22H2-TYPE.
160
C2H2-TYPE.
190
C2H2-TYPE.
219
C2H2-TYPE.
493
C2H2-TYPE.
523
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN HELIOS A).
AD142BD4 CRC32;
                                                                                                                                                          36, CREATED)
36, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
                                                                                                                          Ą.
                                                                                                                          526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00028; ZINC_FINGER_C2H2; 5.
                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
59388 1
                                                                                                                                                                                                            ZINC FINGER PROTEIN HELIOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF044257; G2829277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR
                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
168
196
471
499
111
526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
118; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-BINDING;
                                                                                                                                                                           15-JUL-1998
                                                                                                                                                                                             15-DEC-1998
                                                                                                                          HELI_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S:
Matches 118,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
SEQUENCE
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ZN_FING
ZN_FING
ZN_FING
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ZN_FING
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GEORGOPOULOS K., MOORE D.D.,
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ZN_FING
ZN_FING
VARSPLIC
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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DOMAIN
ZN_FING
ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|| | : | | | | | | | EENGLAIDMAMNGEEEE------ECAEDLRVLDASGAKVNGSHAGGPDSKGPYSSAG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 GIRLPNGKLKCDICGIVCIGPNVLMVHRRSHTGERPFQCTQCGASFTQKGNLLRHIKLHS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 -----GKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 GEKPFKCHLCNYACORRDALTGHLRTHSVEKPYKCEFCGRSYKORSSLEEHKERCRTFLQ 164
         -! SIMILARITY: BELONGS TO THE IKAROS FAMILY OF ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 DENVLKSEPMGNAEEPEIPYSYSREYNEYENIKL------ERHVVSFDSSRPTS--- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INCREMOUSE STANDARD; PRT; 517 AA.

ID IKAR_MOUSE STANDARD; PRT; 517 AA.

AC 003267, 064044; 064061; 064051;

DT 01-0CT-1993 (REL. 27, CREATED)

DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

DI 16-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
                                                                                                                                                                        PROSITE; PS00028; ZINC_FINGER_C2H2; 5.

PFAM: PF00096; Zf-C2H2; 5.

TRANSCRIPTION REGULATION; ACTIVATOR; ZINC-FINGER; METAL-BINDING; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING.

DOMAIN 125 203 ZINC-FINGERS II.

ZN_FING 125 147 C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                    (IN IK-2, IK-4 AND IK-8).
(IN IK-6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKAROS OR LYFI.
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA: SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 CMGLQNSIYTVVKEESNQNEQREDLSQMGSKRALVLDRLANNVAKRKSTMPQKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----STDPGDTASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKF
                                                                                                                                                                                                                                                                                                                                                                                                                         59.9%; Score 675; DB 1; Length 522; 58.1%; Pred. No. 2.8e-53; Live 23; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                           AND IK-8)
                                                                                                                                                                                                                                                                                                                                         (IN IK-5).
(IN IK-4).
(IN IK-3).
                                                                                                                                                                                                                                                       CZHZ-TYPE.
CZHZ-TYPE.
CZHZ-TYPE.
CZHZ-TYPE.
CZHZ-TYPE.
CZHZ-TYPE.
MISSING (IN IK-2,
MISSING (IN IK-6).
AT DAY 5-6 IN THE EMBRYO PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 5)
                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                             EMBL; U92201; G2062742; -.
                                                                                                                                                                                                                                                                                                                                                                                       57657
                                                                                                                                        EMBL, U92200, G2062740, -
EMBL, U92198, G2062736, -
EMBL, U92199, G2062738, -
PROSITE, PS00028, ZINC_FII
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 58.1
Matches 136; Conservative
                                                                                                                                                                                                                                 468
1153
1153
1163
1163
1168
468
468
496
1149
206
206
206
222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=EMBRYO;
MEDLINE; 93068267
                                                                                                                                                                                                                                  DOMAIN
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
WARSPLIC
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: SIX FORMS OF THE PROTEIN, ISOFORMS I-VI, ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE IS THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIATION; ACTIVATOR; ZINC-FINGER; METAL-BINDING;
223 ZINC-FINGERS I.
2105 ZINC-FINGERS II.
2106 C2H2-TYPE.
2106 C2H2-TYPE.
2107 ZINC-TYPE.
2107 C2H2-TYPE.
2108 C2H2-TYPE.
2109 C2H2-TYPE.
211 C2H2-TYPE.
212 C2H2-TYPE.
213 Name of the company of the
                                                                                                                                                                                                                MEDILINE: 95021239.

MEDILINE: 95021239.

HANH K., ERNST P., LO K., KIM G.S., TURCK C., SMALE S.T.;

HANH K., ERNST P., LO K., KIM G.S., TURCK C., SMALE S.T.;

"The lymphoid transcription factor LyF-1 is encoded by specific, alternatively spliced mrnAs derived from the Ikaros gene.";

MOL. CELL. BIOL. 14.7111-7123(1994).

-!- FUNCTION: BIDDS AND AT123(1994).

-!- FUNCTION: BIDDS AND AT123(1994).

-!- FUNCTION: BIDDS AND AT124 THE ENHANCER (DELTA-A ELEMENT) OF THE CD3-DELTA-GENE. FUNCTIONS IN THE SPECIFICATION AND THE MATURATION OF THE LYMPHOCYTE. ALSO INTERACTS WITH A CRITICAL CONTROL ELEMENT IN THE TOT (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) PROMOTER AS WELL AS WITH THE PROMOTERS FOR OTHER GENES EXPRESSED DURING EARLY STAGES OF B AND I CELL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN T-CELLS AND THEIR PROGENITORS, AND ALSO IN B-CELLS.
-!- SIMILARITY: BELONGS TO THE IRAROS FAMILY OF ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                            "Ikaros, an early lymphoid-specific transcription factor and putative mediator for T cell commitment."; SCIENCE 258:808-812(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VC -> MY (IN REF. 2).
MISSING (IN REF. 2).
D18D2D97 CRC32;
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73.7%; Pred. No. 3.7e-52;
tive 15; Mismatches 21
DERFLER B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S/4/10.
MGD; MGI:96535; IKAROS.
PROSITE; PS00028; ZINC_FINGER_C2H2; 4.
PFAM; PF00096; zf-C2H2; 4.
"ccb: P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L03547; G198287; -
EMBL; S74517; G807149; ALT_SEQ.
EMBL; S74518; G807151; -
EMBL; S74708; G807153; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57336 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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54
141
234
480
517 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim:
Matches 126;
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                                                                                                                                                                                                                                                              107 KPFKCHLCNYACQRRDALIGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEUKOCYTES.
DEVELOPMENTAL STAGE: EXPRESSED EARLY IN EMBRYO FROM EMBRYONIC DAY
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE IKAROS FAMILY OF ZINC-FINGER PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC HEMATOPOIETIC ORGANS SUCH AS THE BURSA OF FABRICIUS, THYMUS AND SPLEEN. IN THE ADULT, EXPRESSED IN SPLEEN, THYMUS, BURSA AND PERIPHERAL BLOOD
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ن
                                                                                                                                                                                                                                                                                                                                              167 D-PG-----DIASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKF 209
                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METÀZOA; CHÓRDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                   6
MISSING (IN IK4).
MISSING (IN IK2).
MISSING (IN IK6).
MISSING (IN IK6).
MISSING (IN IK6).
OV -> FS (IN REF. 2).
S -> T (IN REF. 2).
N -> K (IN REF. 2).
N -> K (IN REF. 2).
N -> K (IN REF. 2).
KPLA -> RS (IN REF. 2).
KPLA -> RRS (IN REF. 2).
KPLA -> RRS (IN REF. 2).
KPLA -> RRS (IN REF. 2).
N -> Y (IN REF. 2).
KPLA -> RRS (IN REF. 2).
N -> Y (IN REF. 2).
PHARNGL -> RRAQRY (IN REF. 2).
W; 5A97272D CRC32;
                                                                                                                                                                                               15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                   518 AA
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W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-H.B2; TISSUE-THYMUS;
MEDLINE; 97439462.
                                                                                                                                                                                               Query Match
Best Local Similarity 74.4%
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKAROS OR IK.
GALLUS GALLUS (CHICKEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIIPPO J., LASSILA O.;
                                                                                                                                              420
519 AA;
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O42410;
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TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-SHASTA, TISSUE-THYMOCYTES;
MEDLINE; 99056818.
HANSEN J.D., STRASSBURGER P., DU PASQUIER L.;
"Conservation of a master hematopoietic switch gene during vertebrate evolution: isolation and characterization of Ikaros from teleost and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQ-- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - 171 KPFKCHLCNYACRRRDALIGHLRTHSVGKPHKCGYCGRSYKQRSSLEEHKERCHNYLQTM 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUR. J. IRMUNOL. 27:3049-3058(1997).
-!- FUNCTION: BINDS AND ACTIVATES THE ENHANCER (DELTA-A ELEMENT) OF
THE CD3-DELTA GENE. FUNCTIONS IN THE SPECIFICATION AND THE
MATURATION OF THE T LYMPHOCYTE. ALSO INTERACTS WITH A CRITICAL
CONTROL ELEMENT IN THE TDT (TERMINAL DEDXYNUCLEOTIDYLTRANSFERASE)
PROMOTER AS WELL AS WITH THE PROMOTERS FOR OTHER GENES
EXPRESSED DURING EARLY STAGES OF B AND T CELL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: EIGHT FORMS OF THE PROTEIN; IK1-IK8; ARE
PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE IS THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: EXPRESSION BEGINS AT DAY 3-4 IN THE YOLK SAC
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                                                                                                                                   PROSITE; PS00051 23.211.

PROSITE; PS00096; Z=C2H2; 5.

PFAM; PF00096; Z=C2H2; 5.

PFAM; PF00096; Z=C2H2; 5.

PFAM; PF00096; Z=C2H2; 5.

PFAM; PF00096; Z=C2H2; 5.

DNA=N; PF00096; Z=C2H2; 5.

DNA=N; PF00096; Z=C2H2; Z=CZH2; Z=CZH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 SISSNLYSVIKEETNQSEMAEDLCKIGSERSLVLDRLASNVAKRKSSMPQKF 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND PRONEPHROS. VERY LOW EXPRESSION IN LIVER. TESTIS, BRAIN, EYE AND MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.1%; Score 676.5; DB 1; Best Local Similarity 73.3%; Pred. No. 2.1e-53; Matches 126; Conservative 14; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB4DF123 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
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modified and this statement is not removentities requires a license agreement ((or send an email to license(lsb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-BINDING PROTEIN IKAROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SALMONIDAE; ONCORHYNCHUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                    EMBL; Y11833; E309211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amphibian species.
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IKAR_ONCMY
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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- protein search, using sw model OM protein

(without alignments)
436.020 Million cell updates/sec 6, 1999, 11:46:20 ; Search time 13.55 November uo: Run

US-09-019-348-8 1126 Title: Perfect score:

1 ERDENVLKSEPMGNAEEPEI......VLDRLASNVAKRKSSMPQKF 209

Sequence:

BLOSUM62 Scoring table:

77977 segs, 28268293 residues Searched:

SwissProt_37:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ç		o sapien	gallus gall	orhynchu	musculu	musc	Ο.				Ħ		musculu	taurus						xenopus lae	musculu				drosophila		o sapien	mus musculu				o sapien	o sapien	rattus norv	xenopus lae		o sapien	E	o sapien					o sapien
	scription		3422	2410			1183 mus			8698 homo	5481 homo	7141 mus	1751 mus				5072 homo					_					P15620 mus												1967 mus	2386 homo		9676 hото			7097 homo
	Ď	*********	01	94	01:	8	P8	PO	P2	P2	8	P1	90	PO	02	01	01	8	01	8	P1	8	P5	8	07	P2	P1	P5	8	Pl	PS	PS	01	P1	8	P1	P1	P1	90	8	P1	60	P1	P1	PI
SUMMARIES	ID		IKAR_HUMAN	IKAR_CHICK	IKAR_ONCMY	IKAR_MOUSE	HELI_MOUSE	XFIN_XENLA	ZN43_HUMAN	ZN42_HUMAN	ZN91_HUMAN	ZF37_MOUSE	KID1_MOUSE	KR2_MOUSE	OZF_BOVIN	Z141_HUMAN	OZF_HUMAN	Z11B_HUMAN	Z195_HUMAN	ZN85_HUMAN	ZO28_XENLA	ZF29_MOUSE	Z157_HUMAN	Z33A_HUMAN	Z189_HUMAN	CF2_DROME	ZF35_MOUSE	ZN83_HUMAN	MLZ4_MOUSE	ZG57_XENLA	Z135_HUMAN	Z132_HUMAN	Z177_HUMAN	ZNO8_HUMAN	KID1_RAT	ZOZO_XENLA	ZF26_MOUSE	ž	ZF90_MOUSE	ZN45_HUMAN	2N35_HUMAN	184		ZO6_XENLA	ZNO7_HUMAN
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514 139 167 195 484 514

DOMAIN ZN_FING ZN_FING ZN_FING ZN_FING ZN_FING ZN_FING

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. MOLNAR A., WU P., LARGESPADA D.A., VORTKAMP A., SCHERER S.,
MOLNAR A., WU P., LARGESPADA D.A., UNDERGROPOLIOS K.;
COPELAND N.G., JENKINS N.A., BRUNS G., GEORGOPOLIOS K.;
The Ikaros gene encodes a family of lymphocyte-restricted zinc
finger DNA binding proteins, highly conserved in human and mouse.";
J. IMMUNOL. 156:385-592(1996).
C. I- FUNCTION: BINDS AND ACTIVATES THE ENHANCER (DELTA-A ELEMENT) OF
THE CD3-DELTA GENE. FUNCTIONS IN THE SPECIFICATION AND THE
MATURATION OF THE TLYMPHOCYTE. ALSO INTERACTS WITH A CRITICAL
CONTROL ELEMENT IN THE TDT (TERMINAL DEOXYUGLEOTIDYLTRANSFERASE)
PROMOTER AS WELL AS WITH THE PROMOTERS FOR OTHER GENES EXPRESSED OF B AND T CELL DEVELOPMENT.
C. IS SUBCELLULAR LOCATION: NUCLEAR.
C. ITSSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMUS, SPLEEN AND
PERIPHERAL BLOOD LEUKOCYTES AND LYMPH NODES. LOWER EXPRESSION IN
BONE MARROW AND SMALL INTESTING.
C. INTERNATIVE PRODUCTS: SIX FORMS OF THE PROTEIN; ISOFORMS IXI-IKE;
MARROW AND SMALL INTESTING. THE SEQUENCE SHOWN HERE IS
   P16372 mus musculu
Q62981 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THAT OF IKI.
-!- SIMILARITY: BELONGS TO THE IKAROS FAMILY OF ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
TISSUB-BONE MARROW;
MEDLINE; 9625222.
NIETFELD W., MEYERHANS A.;
"Cloning and Sequencing of hik-1, a cDNA encoding a human homologue of mouse Ikaros/LyF-1.";
IMMUNOL. LETT. 49:139-141(1996).
                                                                                                                                                                                                                                                                                 Or Senu a...

EMBL; 40462; G1289371; -.

EMBL; 80876; G1911483; -.

MIM; 603023; -.

PROSITE; PS000025; Z1-CZH2; 5.

PRAM; PF00096; Z2-CZH2; 5.

TRANSCRIPTION REGULATION; ACTIVATOR; ZINC-FINGER; METAL-BINDING; DNA-BINDING; NUCLEAR PROTEIN; ALT-FINGERS I.

Z24 ZINC-FINGERS I.

S117 Z24 ZINC-FINGERS I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                               ALIGNMENTS
   MFG1_MOUSE
O2F_RAT
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   169
407
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273.5
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IKAR_HUMAN
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A; Title: Second-order repeats in Xenopus laevis finger proteins.
A; Peference number: S05632; MUID: 90040698
A; Status: not compared with conceptual translation
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S
                                                                                     C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C.Accession: G02075
R;Poncelet, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   finger protein (clone XlcOF28) - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-1993
C;Accession: S06556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEH 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 YVKVAHKFSN--SNRHEIRHTKKKP----FKCTKCGKSFGMISCLJEHSRIHTRVNFYKC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YACQ-----RRDALTGHLRTHSVEKPYKCEFCGRSYK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 LERHVVSFDSSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 YSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCG----LSCI------64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---RC-RTFLQSTDPGDTASAEARHIKAEMGSERALVLDRLASNV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
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                                                                                                                                                                     submitted to the EMBL Data Library, September 1995
A;Reference number: G09169
A;Secession: G02075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-595 <PON>
A;Cross-references: EMBL:U35376; NID:g1017721; PID:g1017722
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.5%; Score 287.5; DB 2; Best Local Similarity 36.6%; Pred. No. 6.6e-18; Matches 64; Conservative 28; Mismatches 64;
                                                                  transcription repressor zinc finger protein 85 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.6%; Score 288; DB 2; Best Local Similarity 32.3%; Pred. No. 8.1e-18; Matches 61; Conservative 25; Mismatches 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-439 <NIE>
C; Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:ZNF85
A;Cross-references: GDB:132279
A;Map position: 19p12-19p12
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249 QKTHESKPQQDSPNCEKTFEQESAP-KTATMDQLHESA--GLEKVPELPEATNSV 300

Search completed: November 6, 1999, 08:08:52 Job time: 72 sec .. 2

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finger protein ZNF11B - human (fragment)
C;Species: Homo saplens (man)
C;Accession: S33989;
S;Stydensce_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: S33989;
Mucleic A; Liu, L.; Moore, J.K.; Leversha, M.A.; Jackson, M.S.; Papi, L.; Fer Nucleic Acids Res. 21, 1409-1417, 1993
A;Title: Duplicated KOX zinc finger gene clusters flank the centromere of human chrom A;Reference number: S30238; MUID:93219119
               essentially of zinc finger motifs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTEHBKIHIGEKPFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTSLIVH 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 IKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 VRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGCNECGKAFSQFSTLALHL-RI 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------CDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRH 99
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       A,Title: The OZF gene encodes a protein consisting essenti
A,Reference number: $43826, MUD:94149744
A,Accession: $43826
A,Molecule type: mRNA
A,Residues: 1-292 <LEC>
A,Coss-references: EMBL:X70394, NID:9468707; PID:9468708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DDA
A;Residues: 65-287 <TUZ>
A;Cross-references: EMBL:X68685; NID:9296453; PID:9938236
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Pred. No. 5.1e-18;
0; Mismatches 32
                                                                                                                                                                                                 A)Cross-references: GDB:230289; OMIM:601505
A;Map position: 19q13.1-19q13.1
C;Keywords: DNA binding; zinc finger
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Map position: 10q11.2-10q11.2
Keywords: zinc finger
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A;Molecule type: mRNA
Residues: 1-78 <TUN>
A;Residues: EMBL:X68684
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Best Local Similarity
Matches 50; Conservat
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Best Local Similarity
Matches 62; Conserv
                                                                                                                                                      C;Genetics:
A;Gene: GDB:ZNF146; OZF
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A:Title: A zinc-finger gene ZNF141 mapping at 4p16.3/D4S90 is a candidate gene for the WA; Reference number: 154338; WUID:94093541
A; Accession: 154338
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C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 17-Mar-1999
C:Accession: 543826
R:le Chalony, C.: Prosperi, M.T.: Haluza, R.; Apiou, F.; Dutrillaux, B.; Goubin, J. Mol. Biol. 236, 399-404, 1994
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C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Aug-1997
C:Accession: 154338
                                                                                                                                                                                                                                                                                                                                                                                    111 OSSSLLKHORIHTGEKPYTCNVCDKHFIERSSLTV--HORTHTGEKP----YKCHECGKA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                    62 CISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 : 11 : 11 : 1
202 EECGKAFKWSLIFNEHKRIHTGEKPFTCEECGSIFTTSSHFAKHKIIHTGEKP----YKC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 DVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 EECGKAFNRFTTLTKHKRIHAGEKPITCEECRKIFTSSNFAKHKRIHTGEKPYKCEECG 317
                                                                                                                                                                                                                                                                                                                                      2 RDENVLKSEPMGNAEEPEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCGLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KLERHVVSFDSSRPTSGKMNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 474;
                                                                                                                                                                                                                                                    Length 347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 75-347 <CH2>
A;Cross-references: GB:M15709; NID:g193351; PID:g193352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 YACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-474 <RES>
A;Cross-references: GB:L15309; NID:g347905; PID:g347906
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60;
                                                                                                                                                                                                                                        Query Match 25.8%; Score 290; DB 2; Best Local Similarity 34.8%; Pred. No. 3.1e-18; Matches 54; Conservative 34; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.7%; Score 289; DB 2; Best Local Similarity 34.6%; Pred. No. 5.2e-18; Matches 56; Conservative 22; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 DALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Gene: GDB:ZNF141
A.Cross-references: GDB:137046; OMIM:194648
A:Map position: 4p16.3-4p16.3
A;Reference number: A90892; MUID:87131089
A;Accession: B26595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 EEPEIPYSYSREYNEYENI-------
                                                                                                                                       A:Gene: mKr2
C:Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zinc finger protein - human
                                           A; Molecule type: DNA
A; Residues: 75-347 <CH2>
                                                                                                                     C; Genetics:
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Withtenate names: mixiz

Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

S;Chowdhury, K.; Dressler, G.; Breier, G.; Deutsch, U.; Gruss, P.

R;Chowdhury, K.; Dressler, G.; Breier, G.; Deutsch, U.; Gruss, P.

A;Reference number: S00549; MUD:88312581

A;Reference number: S00549; MUD:88312581

A;Recession: S0054

A;Residues: 1-347 < CHO>

A;Residues: 1-347 < CHO>

A;Residues: L-347 < CHO>

A;Cross-references: EMBL:Y00850; NID:952810; PID:952811

A;Chowdhury, K.; Deutsch, U.; Gruss, P.

Cell 48, 771-778, 1987

A;Title: A multigene family encoding several "finger" structures is present and diffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                      4
                                                                                                                                                                                                                                                                                                        268 KPYECEQCGKAHGHKHALTDHLRIHTGEKPYKCNECGKTFRHSSNLMQHLRSHTGEKPYE 327
                                                                                                                                                                                                                                                                         132 SVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQSTDPGDTASAEARHIKAEMGSERALVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTSGK-MNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
                                      Gaps
                                                                                                                            1015 MHTGEKPYKCEECGKAFN--RSSKLTTHKIIHTGEKP----YKCEECGKAFISSSTLNGH
                                                                                 MGNAEEPEI PY SY SREY NEY EN I KLERHVVSFDSSRPTSGKMNCDVCGLSCISFNVLMVH
                                                                                                                                                                                KRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTH
                                      16;
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                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEH--
                   Pred. No. 3.3e-18;
); Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.1%; Score 294; DB 2; 38.0%; Pred. No. 2.2e-18; iive 29; Mismatches 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKECGKSFRYN-----SSLTEHVRTHTG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 -KERCRIFLQSTDPGDTASAEARHIKAEMG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental control protein Kr2 - mouse
34.9%; Fr. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 38.0%
Matches 57; Conservative
                   Best Local Similarity 34.9
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               finger protein zfp-37 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                   : :! !
1179 ETILANTVK 1187
                                                                                                                                                                                                                                                                                                                                                                      192 DRLASNVAK 200
                                                                                          12
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C;Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: S35305
Bs Bellefroid, E.J.; Marine, J.C.; Ried, T.; Lecocq, P.J.; Riviere, M.; Amemiya, C.; Ponc
BBO J. 12, 1363-1374, 1993
A;Title: Clustered organization of homologous KRAB zinc-finger genes with enhanced expre
A;Reference number: S35305; MUID:93223677
                                                                                                                                                                                                                                                                                                                                                                                                            R;Hromas, R.; Collins, S.J.; Hickstein, D.; Raskind, W.; Deaven, L.L.; O'Hara, P.; Hagen J. Biol. Chem. 266, 14183-14187, 1991
A;Title: A retinoic acid-responsive human zinc finger gene, MZF-1, preferentially express A;Reference number: A40751; MUID:91317761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1191 - GEEL>
A; Cross-references: EMBL:L11672; NID:g186773; PID:g186774
A; Note: the authors translated the codon GCA for residue 750 as Thr and GCT for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                   C:Species: Homo sapiens (man)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 24-Sep-1998
C:Accession: A40751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPY 137
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 PEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTG 77
                       NHCGKVLSHKQGLLDHQRTHTGEKPYECNECGIAFSQKSHLVLHQRTHTGEKPYECEQCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: GDB:125898; OMIM:194550
A:Map position: 19q13.2-19q13.4
C:Keywords: DNA binding; transcription regulation; zinc finger
                                                                       YACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M58297; NID:g189043; PID:g189044
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.4%; Score 297; DB 2;
41.0%; Pred. No. 1.1e-18;
tive 22; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:ZNF91; HPF7; HTF10
A;Cross-references: GDB:13284
A;Map position: 19p12-19p12
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                  164 QSTDPGDTASAEARHIKAEMG 184
                                                                                                                                                                                                                195 YN-----SSLTEHVRTHTG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  zinc finger protein ZNF91 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 KCEFCGRSYKQRSSLEEHK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: ||| : | : | : |: |
461 ACQDCGRRFHQSTKLIQHQ 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Conservative
                                                                                                                                                                                                                                                                                                                              finger protein MZF1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB: ZNF42; MZF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A40751
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-485 < HRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S35305
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                            75
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RiLovering R.; Trowsdale, J.
Nucleic Acids Res. 19, 2921-2928, 1991
Nucleic Acids Res. 19, 2921-2928, 1991
Nucleic Acids Res. 19, 2921-3284
Nucleic A gene encoding 22 highly related zinc fingers is expressed in lymphoid cell A; Reference number: S26823; MulD:91279444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S10245

C;Accession: S10245

Nucleic Acids Res. 18, 3655, 1990

A;Title: Cloning and sequencing of a zinc finger cDNA expressed in mouse testis.

A;Reference number: S10245; MUID:90301500

A;Redexion: S10245

A;Molecule type: mRNA

A;Residues: 1-411 < MEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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                                                                                                                                                                                                               finger protein ZNF43 - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1998
C;Accession: S26823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   finger protein, testis - mouse
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 10-Sep-1997
              GFIQNSDLVKHFRTHTGERPYQCAECHKGFIQKSDLVKHLRTHTGEKPFKCSHCDKKFTE 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCN 115
                                                                                  -KLERHVVSF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
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                                                        121 RDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKE-----RC----RTFLQSTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 411;
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C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 299; DB 2; I
Pred. No. 1.2e-18;
5; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.5%; Score 298.5; DB 2
32.8%; Pred. No. 6.7e-19;
ive 34; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                 A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-803 <LOV>
A:Cross-references: EMBL:X59244; NID:938031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ENVLKSEPMGNAEEPEIPYSYSREYNEYENI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.6%; Scor
35.3%; Pred
tive 26;
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Best Local Similarity 32.8%
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GDB:ZNF43; HTF6
A;Cross-references: GDB:128653
A;Map position: 19pl3.1-19pl2
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S26823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
           362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104
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Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cispecies: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 31-Dec-1993
CiAccession: 500647
Altaba, A.; Perry-O'Keefe, H.; Melton, D.A.
EMBO, J. 6, 3065-3070, 1987
A:Title: Xfin: an embryonic gene encoding a multifingered protein in Xenopus.
A:Reference number: 500647; MUID:88082679
A:Reference number: 500647; MUID:88082679
A:Residue type: mRA
A:Residue type: mRA
A:Residues: 1-1350 cRUL>
A:Residue title: Met-1, Met-11, Met-16, Met-38, or Met-39 is the initiate
Ciscertics:
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GERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKCEFCGRSYKQRSSLEEHKERCRTFLQSTD-PG-----DTASAEARHIKAEMGSERA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 564; DB 2;
Pred. No. 4.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.2%; Score 317.5; DB 2
36.9%; Pred. No. 4.9e-20;
iive 33; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
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Keywords: DNA binding; zinc finger
                                                                    LVLDRLASNVAKRKSSMPQKF 209
                                                                                         LVLDRLASNVAKRKSSMPQKF 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVLDRLASNVAKRKSSMPQKF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.18;
75.98;
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Best Local Similarity 75.9%
Matches 107; Conservative
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Best Local Si
Matches 66;
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GenCore version 4.5
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OM protein - protein search, using sw model

November 6, 1999, 08:08:51; Search time 18:18 Seconds (without alignments) 460:599 Million cell updates/sec Run on:

US-09-019-348-8 1126 1 ERDENVLKSEPMGNAEEPEI......VLDRLASNVAKRKSSMPQKF 209 **BLOSUM62** Title: Perfect score: Sequence: Scoring table:

122810 seqs, 40065486 residues Database : Searched:

pirl:* pir2:* pir3:* pir4:* PIR_60:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	-binding prot	karos DNA bindi	ld tran	inger protein -	inger protein Z	inger protein,	inger proteir	inc finger pr	finger protein zfp	evelopmental	inc finger pro	inger protein	c	ranscription r	rotein	inc finger pro	inger protein	horion transcri	protein	spermatogenesis pr	finger protein (cl		krueppel-related p	zinc finger protei	zinc finger protei	zinc finger protei	finger protein (cl	ت.	۲١	finger protein (cl	inger protein HZ	NK10 prot	ription	finger	zinc finger protei	oinding pro	nger protein Z	inger protein H	ŗ
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Length	m																																						
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9 Ouery Match	59	50	20	28	26	26	26	26	56	25	25	23	23	2	2	2	25	~	2,	5	2	7	2	2	7	7	ñ	ñ	ñ	7	5	ñ	Ň	ñ	Ñ	ñ	Ñ	Ň	Ñ
Score	671		9		6											85.		82.		82.			81.		80.					78						92		75	
Result No.	-	7	e	4	Ŋ	φ	7	ھ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39

137 YKCEFCGRSYKQRSSLEEHKERCRTFLQSTD-PG-----DTASAEARHIKAEMGSERA 188

oy oy

finger protein XFO zinc finger protein mfg finger protein mfg finger protein 2, finger protein (cl finger protein kox		-1995 #text_change 19-Oct-1995 functionally diverse zinc finger DNA-bin eptual translation	tch al Similarity 73.7%; Score 671; DB 2; Length 518; al Similarity 73.7%; Pred. No. 2.6e-51; 126; Conservative 15; Mismatches 22; Indels 8; Gaps 2; RPTSGKMNCDVCGLSCISFNVLMVHRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106 SIMIL	16 23	<pre>ig-1996 #text_change 28-Feb-1997 transcription factor and a putative media dBL/DDBJ PID:g198287</pre>	tch 50.1%; Score 564; DB 2; Length 431; al Similarity 75.9%; Pred. No. 4.7e-42; 107; Conservative 11; Mismatches 15; Indels 8; Gaps 2; GERPFOCNQCGASFTOKGNLIRHIKLHTGEKPEKCHLCNYACQRRDALTGHLRTHSVEKP 136
2 S65088 2 A34612 2 A39240 2 B32891 2 S06577 2 S10397	ALIGNMENTS	1 - mouse ouse) vision 19-Oct 1994 a family of :95059058 red with conc	9.6%; Score 671; DB 2 13.7%; Pred. No. 2.6e-E. ve 15; Mismatches SENVLMVHKRSHTGERPFOCNOC	KPEKCHLCNYACORRDALTGHLRTHSVEKPYKCEFCGRSYKORSSLEEHKE	ise) Salon 02-Au Derfler, B. 1-specific 33068267 from GB/EM	50.1%; Score 564; DB 2; 75.9%; Pred. No. 4.7e-42; ive 11; Mismatches 15 KKGNLLRHIKLHTGEKPFKCHLCNYAC
2 591 2 686 2 651 2 210 1 462		Ikaros form Ilus (house me #sequence_repoules, K. 9822-8303, gene encodes A56355; MUID Y; not comparity hot comparity hot splicing	1arity 73. Conservative INCDVCGLSCISF	YACORRDAL 	protein - mouse ulus (house mouse mouse moore, lesseduence_rev') 2, 1995 1, 1995 159572; MulD: 179; translated NAC: 1885> GB:L03547; NII	larity 75. Conservative NQCGASFTQKGN
24 24 24 24 24 24 24 24 24 24 24 24 24 2		g protein Ikara Mus musculus n: A56355 A: Georgopoul BAO1 14, 829 He Ikaros gene e number: A563 n: A56355 preliminary; n preliminary; n type: mRNA : 1-518 cMOL>	Con KMNCD	HLCNY	binding prot Mus musculus Aug-1996 #see Aug-1995 #see Ilos, K.; Moo Ilos, K.; Moo Ilos, K.; Moo Ilos, K.; Moo Ilos, K.; Moo Ilos, Ilos, Il	ch 1 Similarity 107; Conser ERPFQCNQCGAS
275 273.5 273.5 272.5 271.5		ding proes: Mus. 19-0ct-sion. 19-0ct-sion. 11. Biol. 11. Biol. 11. Biol. 11. Biol. 12. Sion: A5 sion.			SULT 2 ars DNA binding ISPRECIES: Mus muscubate: Mus muscubate: John 1996 Accession: 199572 Georgopoulos, K.; Title: Ikaros, an Reference number: Accession: 19572 Status: prelimina: Molecule type: mR Genetics: Genetics: Genetics: Genetics:	/ Match Local S1 nes 107; 77 GERPE 1111
44444 01020 1043		RESULT 1 A56355 DNA-binding C; Species: W C; Accession: R; Molnar, A-Moll. Cell. B A; Reference A; Reference A; Accession: A; Status: pr A; Molecule t A; Residues: C; Keywords:	Query Ma Best Loc Matches Qy 47		RESULT 2 IS9572 ISACCES DNA binding protein C; Species: Mus musculus (; Caccession: 155572 R;Georgopoulos, K.; Moore Solence 258, 808.812, 199 A;Title: Ikaros, an early A; Reference number: 15957 A, Accession: 159572 A, Accession: 159572 A, Residues: 1-431 cRES- A; Residues: 1-431 cRES- A; Genetics: A;	Query Ma Best Loc Matches Qy 77 Db 54

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Search completed: November
Job time: 68 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid molecules coding for mammalian tumor suppressor proteins and methods for their isolation
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2
                                                                                                                                                                                                                                                        51 GKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFK 110
                                                                                                                                                                                                                                                                                   66 HCEKTFNRKDHLKNHLQTHDPNKISYACDDCGKKYHTMLGYKRH-----LALHSASNGDL 120
                                                                                                                                                                                                 55 CDVCGLSCISFNVLMVHKRSHTGERPFQCN--QCGASFTQKGNLLRHIKLHTGEKPFKCH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 LCNYACQRRDALTGHLRTHSVEK-PYKCEFCGRSYKQRSSLEEHKERCRTFLQSTDPGDT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ERDENVLKSEPMGNAEEPEIPYS-----YSREYNEYENIKLERHVVSFDSSRPTS 50
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                                                                                   20.0%; Score 225; DB 2; Length 676; ilarity 27.9%; Pred. No. 2e-17; Conservative 32; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 667;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic acid molecules coding for m
TITLE OF INVENTION: tumor suppressor proteins and metho
NUMBER OF SEQUENCES: 15
NOWPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,661
                                                                                                                                                                                                                                                                                                                                                                111 CHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEH 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.9%; Score 224; DB 2; ilarity 31.8%; Pred. No. 2.5e-17; Conservative 25; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TCGVC---TLELGSTEVL-LDHLKSHAEEKANQAPRE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 ASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08224482
Patent No. 5837692
GENERAL INFORMATION:
APPLICANT: Mercola, Dan
APPLICANT: Adamson, Elleen D.
TITLE OF INVENTION: Inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08718661
Patent No. 5876972
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 667 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-718-661-2
; MOLECULE TYPE: protein US-08-398-590A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
                                                                                   Query Match
Best Local Similarity
Matches 46; Conserv
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Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-718-661-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-224-482-4
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6, 1999, 09:41:36

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78 ERPFQC -- NQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEK 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 PYKCEFCGRSYKQRSSLEEHKERCRTFLQSTDPGDTASAEARHIKAEMGS .185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFACDICGRKFARS --- DERKRHTKIHLROKDKKADKSVVASSATSSLSS 441
                                                                                                                                                                                                                                                                                                                         SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,482
FILING DATE: 07-APR-1994
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-ME 9913
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
SELEFAX: (619) 535-901
TELEFAX: (619) 535-901
TELEFAX: (619) 535-901
TELEFAX: (619) 535-901
                     NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
CAREESEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7%; Score 210.5; DB 2 36.4%; Pred. No. 6.6e-16; tive 19; Mismatches 46
PDGF by Mammalian EGR
                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 543 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Conservative
                                                                                             STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 676 amino acids
TYPE: amino acid
                         INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 727 amino acids
TYPE: amino acid
                                                                                                                                  ) MOLECULE TYPE: protein
PCT-US95-08429-9
                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-398-590A-40
                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 EQQEGLLSEVNAEKVVGNMKPPKPTKIKKKGVKKTFQCELCSYTCPRRSNLDRHMKSHTD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 SRPISGKMNCDVCGLSCİSFNVLMVHKRSHIGERPFQCNQCGASFIQKGNLLRHIKL-HT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ERDENVLK----SEPMGNAEEPE-----IPYSYSREYNEY---ENIKLERHVVSFDS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 STOPGDTASAEARHIKAEMGSERALVEDRLASNVAK------RKSSM 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 GEKPYECYICHARF--TQSGTMKMHILQKHTENVAKFHCPHCDTVIARKSDL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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NUMBER OF SEQUENCES: 21
COMPUTER READBLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRICATION DATA:
APPLICATION NUMBER: PCT/US95/08429
FILING DATE: 15-JUN-1995
CLASSIFICATION:
APPLICATION NUMBER: US 08/261,680
FILING DATE: 17-JUN-1994
CLASSIFICATION:
CLASSIFICATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 22.4%; Score 252.5; DB 3
Best Local Similarity 28.4%; Pred. No. 1.6e-20;
Matches 66; Conservative 38; Mismatches 91
                                                          APPLICATION NUMBER: PCT/US95/08429
FILING DATE: 15-JUN-1995
FILING DATE: 15-JUN-1995
FILING DATE: 15-JUN-1995
FILING DATE: 17-JUN-1994
CLASSIFICATION NUMBER: US 08/261,680
FILING DATE: 17-JUN-1994
CLASSIFICATION NUMBER: 31,994
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14538A-11-1PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 266-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14538A-11-1PC
TELECOMMUNICATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application PC/TUS9508429 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-543-504.

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US95-08429-5
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PCT-US95-08429-9
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46 SRPISGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKL-HT 104
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                                                                                                                              1 ERDENVLK----SEPMGNAEEPE-----IPYSYSREYNEY---ENIKLERHVVSFDS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 GEKPYECYICHARF--TQSGTMKMHILQKHTENVAKFHCPHCDTVIARKSDL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 STDPGDTASAEARHIKAEMGSERALVLDRLASNVAK------RKSSM 205
                 Length 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/08398590A

Fatent No. 5935811

GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Schoenherr, Christopher J.
TITLE OF INVENTION: Proteins
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 53
CORRESPONDENCE 53

CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
CITY: San Francisco
STATE: California
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: CITICALISE
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,590A
FILING DATE: 03-AAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION WHEER: US 08/103,445
FILING DATE: 06-AUG-1995
ATTONEY/AGENT INFORMATION:
WANDE: ACCURRENT PROPERATION:
ANDER CALLING DATE: DO-AUG-1995
ATTONEY/AGENT INFORMATION:
Query Match
Best Local Similarity 28.4%; Pred. No. 100 91;
Matches 66; Conservative 38; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DGORET NUMBER: A-60897/RFT/RMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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32 ENIKLERHVVSFDSSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 ENIKLERHVVSFDSSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFT 91
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Chaganti, Raju S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 22.9%; Score 258; DB 2; Length 706; Best Local Similarity 38.7%; Pred. No. 3.6e-21; Matches 48; Conservative 18; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,541B FILING DATE: PALING DATE: CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08553541B Patent No. 5882858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTARION UNDRER: 28,678
REFERENCE/DOCKET NUMBER: 0575/
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 278-0400
TELEFAX: (212) 391-052
TELEX: 42253 COOP UI
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : MOLECULE TYPE: protein US-08-553-541B-2
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                                                                                                                                                               152 LEEH 155
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                                                                                                                                                                                                                                                                                  US-08-553-541B-2
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92 QKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSS 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.9%; Score 258; DB 3; Length 706; 38.7%; Pred. No. 3.6e-21; tive 18; Mismatches 54; Indels
                                                            APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Chaganti, R.S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Indels
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: White, John P. REGISTRATION NUMBER: 28.678
REGISTRATION NUMBER: 43771-A-PCT
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAX: (212) 664-0525
TELERX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/074,967
FILING DATE: 09-UUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application PC/TUS9508429 GENERAL INFORMATION:
APPLICANT:
PCT-US94-06669-2

Sequence 2, Application PC/TUS9406669

GENERAL INFORMATION:
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NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 706 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
LENGTH: 706 amino ac
                                                                                                                                                                                          ADDALL
STREET: 30 ...
                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                            STATE: New 1
COUNTRY: Un
ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: |
LKSH 648
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PCT-US95-08429-5
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59 GLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYAC 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 SQSSKLHIHQRWHTGEKPYECEECGMSFSQRSNLHIHQRWHTGERPYKCGECGKGFSQSS 360
                                                                                                                                                                                                                                                                                                                           6 VLKSEPMGNAEEPEIPYSYSREY-----NEYENIKLERHVVSFDSSRPTSGKMNCDVC 58
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Patent No. 5641672

GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Chagantl, R.S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bc1-6
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                                                                                                                                                                                                      Length 488;
                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 D------HIKAEMGSE 186
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                                                                                                                                                                                               ; Score 263; DB 2;
; Pred. No. 5.6e-22;
41; Mismatches 72,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Milte, John P.
REGISTRATION NUMBER: 28.678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPHONE: (212) 664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                   23.4%;
28.1%;
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                             62; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
                                             BRSTNOT03
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
             IMMEDIATE SOURCE:
                                          ; LIBRARY: BRST
; CLONE: 641127
US-08-933-750C-17
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US-08-074-967-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 HIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHK 156
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                                                                                                                                                                                                                                                                                                                                                                            23.9%; Score 269; DB 2; Length 711; 40.7%; Pred. No. 2e-22; tive 22; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Ye, Henryi
APPLICANT: Ye, Henryi
APPLICANT: Ye, Henryi
APPLICANT: Corley, Nail C.
TITLE OF INVATION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastEN: DOS
SOFTWARE: FastEND for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOWN: ATTOMIC ATTOMIC ATTOWN: ATTOMIC ATTOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08933750C
Patent No. 5932442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEPHONE: (202) 293-7060
TELEX: (491103
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.9%;
Best Local Similarity 40.7%
Matches 48; Conservative
                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-820-170A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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STATE: CA
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US-08-933-750C-17
                                                                                                                                                                                                                      TOPOLOGY:
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51 GKMN-CDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 KKQHICDECGKHFSQGSALILHQRIHSGEKPYGCVECGKAFSRSSILVQHQRVHTGEKPY 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 RIENGALAPKQELPSALESHEVPGTLSMGVPQIFKYGETCFPKGRFER-----KRNPSR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RDEN----VLKSEPMGNAEEPEIPYSYSR-----EYNE--YENIKLERHVVSFDSSRPTS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 KCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKER 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUTRY: United States
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Sughrue, Mion, Zinn, Macpeak & Seas
2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.2%; Score 272; DB 2; Best Local Similarity 35.5%; Pred. No. 3.5e-23; Matches 60; Conservative 29; Mismatches 62)
       FastSEQ for Windows Version 2.0
                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                            UMBER: US/08/933,750C
September 23, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08820170A
Fatent No. 5831058
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Takeshi, WATANABE
APPLICANT: Masato, HORIE
APPLICANT: Toyomasa, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        14:
                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: September
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LIBRARY: MMLR3DT01
; CLONE: 569710
US-08-933-750C-14
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CITY: Washington
                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: line
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US-08-820-170A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 NYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQSTDPGDTASA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 GRIFNDRSAISQHLRTHIGAKPYKCQDCGKAFRQSSHLIRH------QRIHTGERPYA 305
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lial, Preeti
APPLICANT: Lial, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
TUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 CNKCGKAFTQSSH-LIGHQRTHNRTKRKKQP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 EARHIKAEMGSERALVLDRLASNVAKRKSSMP 206
                                                                                                                                                                                                                                                                                                  PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-933750C-14; Sequence 14, Application US/08933750C; Patent No. 5932442; GENERAL INFORMATION:
                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 37.5%
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: HMC1NOT01
CLONE: 9337
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Incyte Pharmaceuticals, Inc
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APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)227-740
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRRACESISTICS:
                                                                Sequence 5, Application PC/TUS9308743
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 568 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 74.3%
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US93-08743-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM
MEDIUM TYPE: Disketi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
STATE: CA
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                            RESULT 3
PCT-US93-08743-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-933-750C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 KPFKCHLCNYACQRRDALIGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
D-PG-----DIASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKF 209
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                                                                                                 RESULT 2
PCT-US95-09345-13
Sequence 13, Application PC/TUS9509345
Sequence 13, Application PC/TUS9509345
FEBERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STREET: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
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Best Local Similarity 73.3%; Pred. No. 1.4e-69;
Matches 126; Conservative 14; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-UULY-94
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAX-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
DPTOM APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
APPLICATION NUMBER: US 05/95
REFERENCE/DOCKET NUMBER: MGP-027PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517,227-1400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 470 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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47 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106 107 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166 8; Gaps TITLE OF INVENTION: IRAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 152

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII 167 D-PG-----DTASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKF 209 60.3%; Score 679; DB 3; Length 568; 74.3%; Pred. No. 2e-69; Live 15; Mismatches 21; Indels 21; Indels Sequence 4, Application US/08933750C
Patent No. 5932442
GENERAL NO. 5932442
GENERAL NO. FUNFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:

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47 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.3%; Score 679.5; DB 2; Best Local Similarity 73.3%; Pred. No. 1.4e-69; Matches 126; Conservative 14; Mismatches 23;
449
109
60
470
479
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BOSTON
STATE: MASSACHUCETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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  17.1
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  192.5
187.5
182
171
171
170.5
  RESULT
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Seguence 13, Appl
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157.247 Million cell updates/sec
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Sequence 2, A
Sequence 62,
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Sequence 3,
Sequence 3,
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1 ERDENVLKSEPMGNAEEPEI......VLDRLASNVAKRKSSMPQKF 209
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Sequence 4,
Sequence 8,
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Sequence 2,
Sequence 9,
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Sequence 2,
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Sequence 2
Sequence 6
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2: /cgn2_6/ptodata/l/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/l/iaa/PcTUS9_COMB.pep:*
4: /cgn2_6/ptodata/l/iaa/backfilesl.pep:*
                    GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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US-08-933 - 750C - 4
US-08-933 - 750C - 4
US-08-933 - 750C - 14
US-08-933 - 750C - 17
US-08-94 - 0669 - 2
PCT- US95 - 08429 - 5
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US-08-224 - 482 - 4
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US-08-466 - 344 - 1
US-08-466 - 344 - 1
US-08-466 - 344 - 8
US-08-456 - 907 - 4
US-08-456 - 907 - 4
US-08-456 - 907 - 4
US-08-456 - 907 - 3
US-08-456 - 907 - 3
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                                                                                                sw model
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                                                                                                protein search, using
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Match Length
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Sequence 4, Appli
Sequence 11, Appl
Sequence 786, App
Sequence 2, Appli
Sequence 9, Appli
Sequence 3, Appli
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Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: GO STATE STREET, Suite 510
CITY: BOSTON
US-08-102-942A-4
US-08-224-482-11
US-08-117-952-786
US-08-946-241B-2
US-08-946-241B-9
US-08-523-376-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: FLOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: ASCII (taxt)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERRUCE/DOCKET NUMBER: 35,695
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICAT
                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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LENGTH: 470 amino acids
TYPE: amino acid
STRANDEDNESS: single
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; FRAGMENT TYPE: C-terminal
US-08-465-590-153
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Length 470; Indels

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This is the amino acid sequence of murine Ikaros protein isoform mix-1, deduced from a cDNA clone (see v42808) obtained from a contained from a contained from a contained from a contained from a cutivating the CD3-delta gene enhancer (see v42804). Proteins a ctivating the CD3-delta gene enhancer (see v42804). Proteins of the murine Ikaros family (see also W70963 and W70965-68) are isoforms that arise from differential splicing of Ikaros gene transcripts, and contain different combinations of zinc fingers. They are expressed primarily in T cells in the adult and may play a crole as a genetic switch regulating entry into the T cell lineage. The murine and human sequences (see W70964, W70969 and W70971) are very similar. The invention provides Ikaros nucleic acids, vectors and host cells expressing Ikaros polypeptides. These can be used to treat T and B cell diseases (e.g. immune deficiencies caused by curys, radiation or cancer), to control expression of heterologous contains contains and provides contains the contains 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treat nervous system diseases (e.g. Alzhelmer's disease) and to modulate cell division, amplification or differentiation, especially in haematopoietic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences. Sequence 518 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and to control cell differentiation
                                        Location/Qualifiers
119. .139
/note= "zinc finger motif"
147. .167
                                                                                                                           /note= "zinc finger motif"
175. 195
/note= "zinc finger motif"
203. .224
                                                                                                                                                                                                                  "zinc finger motif"
                                                                                                                                                                                                                                                          'note= "zinc finger motif"
                                                                                                                                                                                                                                                                                                       "zinc finger motif"
Alzheimer's disease; therapy; diagnosis.
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                                                                                                                                                                                                                                                                              491. .5.
/note=
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05-SEP-1996; US-711417.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Georgopoulos K;
WPI; 98-378292/33.
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Ouery Match 59.4%; score 669; DB 1; Length 518;
Best Local Similarity 73.7%; Pred. No. 4.6e-59;
::atchcs 126; Conservative 15; Mismatches 22; Indels 8; Gaps 2;
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- - DD 171 KPFKCHLCNYACRRDALIGHLRITHSVGKPHKCGYCGRSYKQRSSLEEHKERCHNYLESS 130

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RESULT 15
R92014
ID R92014 standard; Protein; 431 AA.
AC R92014;
DT 08-MAY-1996 (first entry)
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Murine Ikaros protein mIk-2.

W ikaros; transgenic transgenic animal; transgenic mouse; lymphocyte;

KW animal model; mIk-2.

KW animal model; mIk-2.

KW animal model; mIk-2.

KW animal model; mIk-2.

KW musuculus.

KW MOS 604372-A1.

KOS 62 52 540L-1995; U09345.

PE 29-JUL-1994; US-283300.

PE 29-JUL-1994; US-283300.

PE 29-JUL-1995; U09345.

PE 29-JUL-1995; U09345.

PE 29-JUL-1995; U09345.

PE 29-JUL-1995; US-283300.

PE 6EFED 1966.

REP 7 Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine of Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine of Transgenic rodent having Ikaros protein is a master requilator of the sequence of 48 kDa mouse Ikaros protein is a master requilator of the matupoletic differentiation and a major determinant in lymphocyte of Ifferentiation of Ikaros gene transcripts. Transgenic conduction that alters the DNA binding domain of the Ikaros protein, cransgenic an uterion that alters the DNA binding domain of the Ikaros protein, cransgenic are used as models to determine the effects of treatments for immune or sequence 431 AA;

Query Match 49.2%; Score 554; DB 1; Length 431;
Best Local Similarity 75.2%; Pred. No. 1.2e-47;
Matches 106; Conservative 11; Mismatches 16; Indels 8; Gaps
Qy 77 GERPFQCNQCGASFTQKGNLLRHIKLHTGERPFKCHLCNYACQRRDALTGHLRTHSVEKP 136

3

D 54 GERPFQCNQSGASFTQKGNLLRHIKLHSGEKPFKCHLCNYACRRDALTGHLHHHHHH H1 09 137 XKGEFGGRSYKQRSSLEEHKERCRTFLQSTD-PG------DTASAEARHIKAEMGSERA 188

D 114 HKCGYCGRSYKQRSSLEEHKERCHNYLESMGLPGVCPVIKEETNHNEMAEDLCKIGAERS 173

OY 189 LVLDRIASNVARRKSSMPOKF 209
174 LVLDRIASNVARRKSSMPOKF 194

Search completed: November 6, 1999, 06:55:01 Job time: 83 sec us-09-019-348-8.rag

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W70966;
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W72674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders. Disclosure: Fig 4: 102pp; English.

The sequence of 57.5 Kpa mouse Ikaros protein mIK-1 (R92017) was deduced from mouse Ikaros cDNA (T16662) isolated from a mature T-cell line E15 library. Ikaros protein is a master regulator of hematopoletic differentiation and a major determinant in lymphocyte differentiation and a major determinant in lymphocyte differentiation of major determinant in lymphocyte differentiation and a major determinant in lymphocyte differentiation and a major determinant in lymphocyte from differential splicing of Ikaros gene transcripts. Transgenic animals, esp. mice, having a mutated Ikaros transgene, esp. a mutation that alters the DNA binding domain of the Ikaros protein, are used as models to determine the effects of
                                                    09-MAY-1996 (first entry)
Murine Ikaros protein mIk-1.
Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte; immunocomprised; immune system disorder; nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.4%; Score 669; DB 1; Length 518; 73.7%; Pred. No. 4.6e-59; Live 15; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treatments for immune or nervous system disorders. Sequence 518 AA;
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/note- "zinc finger domain F6"
                                                                                                                                         119. .140
/label= F1
/note= "zinc finger domain F1"
/label= F2
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/note= "zinc finger domain F3"
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                                                                                                                                                                                              /note= "zinc finger domain F2"
175. .195
                                                                                                                             Location/Qualifiers
                              R92017 standard; Protein; 518 AA.
                                                                                                                                                                                                                                                                                 460. .480
/label= F5
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(GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                                                                                                                                                                    .513
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                                                                                                    model; mik-1.
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Matches 126; Conserv
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WPI; 96-129389/13.
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                                                                                                                Mus musculus
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The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFKB element on an KRA sequence; (b) it binds to any of a delta A element, an NFKB element or an itaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a cautrally occurring itaros isoform to any of a delta A element. an NFKB element or an itaros binding oligonucleotide consensus sequence; (d) it competitively inhibits itaros binding to itaros responsive elements, or (e). it inhibits protein protein interactions of transcriptional complexes formed with naturally occurring itaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFKB elements and/or itaros-binding oligonucleotides, bind to delta A elements, NFKB elements and/or itaros-binding oligonucleotides, competitively inhibit binding of naturally occurring itaros isoforms to delta A elements, NFKB elements and/or itaros-binding oligonucleotides, competitively inhibit itaros and/or itaros-binding oligonucleotides, competitively inhibit itaros binding to itaros-binding oligonucleotides, competitively inhibit itaros binding to itaros-responsive elements and/or itarios competition it protein protein interactions of transcriptional complexes and/or itarios competition in the control of control of competition in the control of competition in the control of control of control of competition in control of control o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 RLPNGKLKCDICGIVCIGPNVLMYHKRSHTGERPFQCNQSGASFTQKGNLLRHIKLHSGE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS; Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ikaros poly:peptide(s) - useful for treating disorders of immune system or corpus striatum
Claim 1; Column 61-66; 111pp; English.
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Mouse Ikaros isoform mIk-1.
Ikaros; mIK-1; transcription factor; mouse; lymphocyte; cell differentiation; T cell; cancer; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.4%; Score 669; DB 1; 73.7%; Pred. No. 4.6e-59;
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W72674 standard; Protein; 518 AA.
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20 CGT-1998.
05-UW-1995; 465590.
02-WAY-1994; US-238212.
14-SEP-1992; US-946533.
14-SEP-1993; US-465590.
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Best Local Similarity
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WPI; 98-582621/49.
N-PSDB; V66971.
                                                                                                                                  Mouse Ikaros mik-1
                                                                                  14-JAN-1999
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RESULT

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Misc_difference
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                                                                                                                                                                                                                                 'the codon for Gly-232 may be made degenerate to provide a stop codon in recombinant genes of a degenerate library"
                                                                                           "the codon for Pro-187 may be made degenerate to provide a stop codon in recombinant genes of a degenerate library"
/label= Gly, Ala, Val, Ile, Leu, Ser, Thr
/note= "residue 184 may also not be present"
                                                                                                                                                                                                                                 'note= "the codon
                                                      /note= "variable"
187
                                       note- "variable"
                                                                                                                                                  "variable"
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Misc_difference 285
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300
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Misc_difference 375
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                                                    Misc_difference 186
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Disclosure: Page 59-60: 158pp; English.

Disclosure: Page 50-60: 158pp; English.

This is an example of a potential Ikaros sequence derived from a degenerate library of polypeptides based on the amino acid sequences of human and murine Ikaros isoform I proteins hik-1 (see W70964) and mik-1 (see W70966). A combinatorial library is produced using a degenerate library of genes which each include at least a portion of potential likaros sequences. It can be generated by combinatorial intares sequences. It can be generated by combinatorial integenesis at the nucleic acid level.

Native Ikaros is active in the early stages of lymphocyte of ifferentiation. Different isoforms arise from differential splicing of Ikaros gene transcripts. They are expressed primarily in T cells in the adult and may play a role as a genetic switch in T cells in the adult and may play a role as a genetic switch in T cells in the adult and may play a role as a genetic switch in T cells in the adult and may play a role as a genetic switch in T cells in the adult and may play a role as a genetic switch.

Transcripts of Karos and host cells. These can be used to treat I and B cell diseases (e.g. immune deficiencies caused by drugs, and B cell diseases (e.g. immune deficiencies caused by drugs, and be cancer), to control expression of heterologous genes 107 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166 47 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106 Gaps WPI; 98-378292/33.

New nucleic acid encoding Ikaros protein involved in early
New nucleic acid encoding Ikaros protein involved in early
differentiation of lymphocytes - existing in several isoforms, and
related products, used to treat e.g. immune diseases or cancer and
to control cell differentiation radiation or cancer), to control expression of heterologous genes placed under control of an Ikaros-responsive element, to treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, amplification or differentiation, especially in haematopoietic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences. Sequence 470 AA; D-PG-----DTASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKF 209 180 GLPGXXXPVIKEETXHXEMAEDLCKIGXERSLVLDRLASNVAKRKSSMPQKF 231 DB 1; Length 470; 23; Indels 60.1%; Score 676.5; DB 1 72.7%; Pred. No. 7.3e-60; ive 15; Mismatches 23 /note= "variable" Misc_dlfference 432 /note= "variable" 467 "variable" "variable" "variable" "note= "variable" /note= "variable" "variable "variable 'note= "variable' 05-MAR-1998. 02-JAN-1997; 194256. 05-SEP-1996; US-711417. (GEHO) GEN HOSPITAL CORP. Best Local Similarity 72.7 Matches 125; Conservative /note= ' 384 /note= 397 /note= note= note-Misc_difference 430 Misc_difference 431 Misc_difference Misc_difference Misc_difference Misc_difference Misc_difference Misc_difference Georgopoulos CA2194256-A

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Misc_difference 184
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                                                                                                                                                                                                                                        Ikaros poly:peptide(s) - useful for treating disorders of immune
PS Tayan 1: Column 127-130; Illpp; English.

Cainn 127-130; Illpp; English.

The present invention describes a purified peptide having at least one
CC of the following properties: (a) it stimulates transcription of a DNA
Sequence under the control of a delta A element, an NFKB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of
C a delta A element, an NFKB element or an Ikaros binding oligonucleotide
CC consensus sequence; (c) it competitively inhibits the binding of a
CC adurally occurring ikaros isoform to any of a delta A element, an NFKB
C competitively inhibits Ikaros binding to Ikaros responsive element; or
CC formed with naturally occurring ikaros isoforms. The proteins, provided
C that they stimulate gene transcription under the control of delta A
CC delta A elements and/or Ikaros-binding oligonucleotides,
CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,
CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,
CC competitively inhibit binding of naturally occurring Ikaros isoforms of
CC inhibit protein-protein interactions of transcriptional complexes with
CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,
CC inhibit protein-protein interactions of transcriptional complexes with
CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,
CC inhibit protein-protein interactions of transcriptional complexes with
CC disorders, e.q. leukaemia or ALDS, or corpus striatum disorders, e.g.
CA isorders, e.q. leukaemia or ALDS, or corpus striatum disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease. The present sequence represents an Ikaros protein general formula from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 KPFKCHLCNYACRRRDALTGHLRTHSVGKPHKCGYCGRSYKQRXSLEEHKERCHNYLESM 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ikaros zinc finger protein isoform IK-1.
Ikaros; zinc finger; protein; immune disorder; therapy; treatment;
corpus striatum; regulatory gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 470;
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        /note= "any amino acid"
Misc_difference 467
                                          'note= "any amino acid"
                                                                            "any amino acid"
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/label= Exons 1/2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                    14-SEP-1993; US-121438.
05-JUN-1995; US-465590.
(GEHO ) GEN HOSPITAL CORP.
                                                                            /note=
                                                                                                                                     02-MAY-1994; US-238212.
                                                                                                                                                     US-946233
Misc_difference 432
                                                          Misc_difference 469
                                                                                                                                                                                                                 Georgopoulos K;
WPI; 98-582621/49.
                                                                                                                     05-JUN-1995;
                                                                                                                                                    14-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
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Georgaperuca. 1. WPI: 94-118387/14.

T-cell pathway regulatory gene, Ikaros - encodes family of unique zinc finger proteins, useful for treating immune system disorders Claim 14: Figure 4: 112pp: English.

The Ikaros gene encodes a zinc finger protein which can be used in a therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is at disorder. It may also be used for assessing whether a subject is at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "the codon for Ser-145 may be made degenerate to provide a stop codon in recombinant genes of a degenerate library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degenerate to provide a stop codon in recombinant genes of a degenerate library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                risk for an immune disorder. It is of particular use in treating disorder of the corpus striatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ikaros isoform 1 consensus.
Ikaros; mIK-1; hIR-1; transcription factor; mouse; human;
Iymphocyte; cell differentiation; T cell; cancer;
immunodeficiency; Alzheimer's disease; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Gly, Ala, Val, Ile, Leu, Ser, Thr
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Pred. No. 5.2e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches
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                                                                        248 . 288
/label= Exon 5.
289. 333
                                                                                                                       289. .333
/label= Exon 6.
334. .568
54. .141
/label- Exon 3.
                                         142. .247
/label= Exon 4.
                                                                                                                                                                                                            /label= Exon 7
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14-SEP-1992; US-946233.
(GEHO ) GEN HOSPITAL CORP.
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Matches 127; Conservative
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Misc_difference 407
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                   Misc_difference
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         Georgopoulos K;

WPI: 96-129389/13.

Transgenic rodent having Ikaros trans-gene (pref. mutated) - is

Transgenic rodent having Ikaros trans-gene (pref. mutated) - is

Transgenic rodent having Ikaros trans-gene das model to determine

effects of treatment for immune and nervous system disorders

Disclosure; Page 75-76; 102pp; English.

The sequence of an Ikaros protein (R92021) is provided in the

specification. Ikaros protein (R92021) is provided in the

specification. Ikaros protein and amajor determinant in lymphocyte

chematopoietic differentiation and a major determinant in lymphocyte

differentiation. Isoforms of Ikaros gene transcripts. Transgenic animals,

cref. mice, having a mutated Ikaros protein, are used as

models to determine the effects of treatments for immune or nervous
                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "14-JAN-1999 (first entry)
Ikaros protein general formula.
CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
differentiation marker; immune system; corpus striatum; AIDS;
Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                          47 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
                                                                                                                                                                                                                                                                                                                                                                              KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                  ,
6
                                                                                                                                                                                                                                                                                                                         60.3%; Score 679.5; DB 1; Length 470; 73.3%; Pred. No. 3.6e-60; iive 14; Mismatches 23; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 D-PG-----DTASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKF
                 430. .432
/note= "unidentified amino acids'
/note= "unidentified amino acid"
misc_difference 430. .432
                                                  amino acid"
                                                                      /note= "unidentified amino acid"
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Misc_difference 194
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                                                 /note= "unidentified
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Misc_difference 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W72678 standard; Protein; 470 AA.
W72678;
                                                                                                                                                                                                                                                                                                                            Query Match 60.3%
Best Local Similarity 73.3%
Matches 126; Conservative
                                                                                                    28-JUL-1995; U09345.
29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note-
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                                                           misc_difference 469
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                                       misc_difference 467
                                                                                                                                                                                                                                                                                   system disorders.
Sequence 470 AA;
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W72678
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Mew nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and differentiation of lymphocytes - existing in several isoforms, and teated products, used to treat e.g. immune diseases or cancer and to control cell differentiation.

This is the amino acid sequence of human Ikaros protein isoform Ika', deduced from a cDNA clone (see V42840) obtained from a Jurkat T cell line CDNA library. Native Ikaros is active in the acity stages of lymphocyte differentiation, binding to and activating the CD3-delta gene enhancer (see V4280). Proteins of the human Ikaros family (see also W70864 and W70869) are civating the CD3-delta gene enhancer (see V42804). Proteins of the human Ikaros family (see also W70864 and W70869) are isoforms that arise from differential splicing of Ikaros gene isoforms that arise from differential splicing of Ikaros gene isoforms that arise from differential splicing of Ikaros gene isoforms that arise from differential splicing of Ikaros gene isoforms that arise from differential splicing of the human and murine sequences (see also W70865 and W70865-68) are very similar. The invention provides Ikaros mucleic acids, wectors and host cells expressing Ikaros polypeptides. These can be used to treat rervous system diseases (e.g. immune deficiencies caused by the treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, amplification or differentiation, especially in haematopoietic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences.
Human Ikaros isoform hik'i.
Ikaros, hIK'1; transcription factor; human; lymphocyte;
cell differentiation: T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                               "zinc finger motif"
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                                                                                                   W70971 standard; Protein; 516
                                                                                                                                     (first entry)
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489..5
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175. .1
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147. .1
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ub-seP-1996; US-711417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scorgopoulos K;
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                                                                                                                                    11-JAN-1999
Human Ikaros
                                                                                                                                                                                                                       Homo sapiens.
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W70971
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 Length 516;
                                      Indels
DB 1;
Query Match 60.6%; Score 682.5; DB 1
Best Local Similarity 73.8%; Pred. No. 2.1e-60;
Matches 127; Conservative 16; Mismatches 20
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47 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106 g

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KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166 107 õ

misc_difference 407

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171 KPFKCHLCNYACRRRDALTGHLRTHSVGKPHKCGYCGRSYKQRTSLEEHKERCHNYLESM 230
                                                                                                                                    Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte;
immunocomprised; immune system disorder; nervous system disorder;
                               D-PG-----DTASAEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid"
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                                                                                            R92021 standard; Protein; 470
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/note= "...
71
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                                                                                                                            Ikaros protein
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167 D-PG----
                                                                                                                                                                                            Homo sapiens.
                                                                                            11-JAN-1999
                                                                                                                Human Ikaros
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a purified peptide having at least one of the present invention describes a purified peptide having at least one of the present invention describes a purified peptide having at least one of the present invention describes a purified peptide having at least one of a delta A element an NFWB element or an NFWB element or an NFWB element or an IKRB element, and NFWB element or an IKRB elements and/or IKRB elements and/or IKRB elements and/or IKRB elements and/or IKRACS-binding oligonucleotides, bind to delta A elements, NFKB elements and/or IKRACS-binding oligonucleotides, competitively inhibit binding of maturally occurring IKAROS isoforms to delta A elements, NFKB elements and/or IKAROS-binding oligonucleotides, competitively inhibit IKAROS binding to IKAROS-responsive elements and/or inhibit protein interactions of transcriptional complexes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      occurring Ikaros isoforms, can be used to treat immune system
116 KPFKCHLCNYACRRRDALTGHLRTHSVGKPHKCGYCGRSYKQRTSLEEHKERCHNYLESM 175
                                                                                                                                                                                                                                                             CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLPNGKLKCDICGIICIGPNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHSGE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's disease. The present sequence represents a specifically claimed human Ikaros protein.
Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ikaros poly:peptide(s) - useful for treating disorders of immune
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                                                                          60.6%; Score 682.5; DB 1; Length 461;
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; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                     US-121438.
US-465590.
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02-MAY-1994; US-238212.
                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-1992; US-946233
                                                                                                                                                                                                                                                                                                         Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                        Homo sapiens.
US5824770-A.
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05-JUN-1995;
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Best Local Simi
Matches 127; (
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                                                                                                                                                     RESULT
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New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and additional acid encoding Ikaros protein involved in early adifferentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and to control cell differentiation

This is the amino acid sequence of human Ikaros protein isoform of this is the amino acid sequence of human Ikaros protein isoform hir-1, deduced from a CDNA library. Native Ikaros is active in the early stages of lymphocyte differentiation, binding to and activating the CD3-delta gene enhancer (see V42804). Proteins contivating the CD3-delta gene enhancer (see V42804). Proteins contivating the acid ferential splicing of Ikaros gene isoforms that arise from differential splicing of Ikaros gene transcribts, and contain different combinations of zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQST 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             They are expressed primarilly in Teells in the adult and may play a role as a genetic switch regulating entry into the T cell lineage. The human and murine sequences (see also W70963 and W70965-68) are very similar. The invention provides Ikaros nucleic acids, vectors and host cells expressing Ikaros polypeptides. These can be used to treat T and B cell diseases (e.g. immune deficiencies caused by drugs, radiation or cancer), to control expression of heterologous genes placed under control of an Ikaros responsive element, to treat mervous system diseases (e.g. Alzheiner s' disease) and to modulate cell division, amplification or differentiation, especially in haematopoletic cells. Some Ikaros isoforms are antagonistic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                      Ikaros; hIK-1; transcription factor; human; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis.
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W70964 standard; Protein; 461
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Best Local Similarity 73.00,
-hes 127; Conservative
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434
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05-SEP-1996; US-711417.
(GEHO ) GEN HOSPITAL CORP.
                                                               (first entry)
                                                                                            isoform hik-1
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WPI; 98-378292/33.
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Georgopoulos K;
WPI; 96-129389/13.
N-PSDB; T16060.
                         N-PSDB; Q44980
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                                                                                                                                                                                                                                                                                                                                                 Tand lymphoma(s)

Stoclosure; Page 76-78; 115pp; English.

Wouse Abiolos (W15574) is a homologue of Ikaros whose expression is bisclosure; Page 76-78; 115pp; English.

Chouse Abiolos (W15574) is a homologue of Ikaros whose expression is restricted to lymphoid lineage. Its amino acid sequence was deduced from a cDNA clone (T60490) obtd. from a mouse spleen cDNA library. A human Aiolos partial polypeptide has also been identified (see also W15575). Aiolos forms homodimers that are content transcriptional activators. It also forms less potent content contents with Ikaros. Recombinant Aiolos can be produced in transformed host cells. Aiolos misexpressing immune system of components can be used to reconstitute the immune system of a mammal. The Aiolos protein, coding sequence or cells expressing contents.

Cherapy. Such disorders include T-cell leukaemias and lymphomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 RDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRTFLQSTDPGDTASAEARHIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERDENVLKSEPMGNAEEPEIPYSYSREYNEYENIKLERHVVSFDSSRPTSGKMNCDVCGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-OCT-1994 (first entry)
Peptide with Ikaros protein activity.
Praros: Jnc finger; protein; immune disorder; therapy; treatment; corpus striatum; regulatory gene.
Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                Aiolos polypeptide and corresponding DNA - used to reconstitute a mammalian immune system, for the treatment of T cell leukaemia(s)
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                                          290. .344
/label= Activation_domain
/note= "conserved activation domain of Aiolos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 AEMGSERALVLDRLASNVAKRKSSMPQKF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AEMGSERALVLDRLASNVAKRKSSMPQKF 209
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                         Location/Qualifiers
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                                                                                                                                                                                                                                              Georgopoulos K, Morgan BA;
WPI; 97-245047/22.
                                                                                                                                                   17-OCT-1996; U16774.
18-OCT-1995; US-005529.
14-MAY-1996; US-017646.
(GEHO ) GEN HOSPITAL CORP.
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(GEHO ) GEN HOSPITAL CORP.
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14-SEP-1993; U08743.
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Best Local Similarity
Matches 187; Conserv
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                                                                                                                                                                                                                                                                                           N-PSDB; T60490
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Mus sp
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Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine of fetests of treatment for immune and nervous system disorders bisclosure; Fig 2: 102pp; English.

In almost fall-length cDNA sequence (T16060) codes for Part (R92015) of the human Ikaros protein, a zinc finger protein that is a master regulator of haematopoietic differentiation and a major determinant in lymphocyte specification and development. Different isolated Transgenic animals, pref. mice, having a mutated Ikaros transgene, esp. a mutation that alters the DNA binding domain of the Ikaros protein, are used as models to determine the effects of treatments for immune or nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 RLPNGKLKCDICGIICIGPNVLMVHRRSHTGERPFQCNQCGASFTQKGNLLRHIKLHSGE 189
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T-cell pathway regulatory gene, Ikaros - encodes family of unique zinc finger proteins, useful for treating immune system disorders Claim 14; Page 44-46; 112pp; English.

The ikaros gene encodes a zinc finger protein which can be used in a therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is at risk for an immune disorder. It is of particular use in treating a disorder of the corpus striatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFOCNOCGASFTOKGNLLRHIKLHTGE 106
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Human Ikaros protein hIk-1.
Ikaros; transgene; transgenic animal; transgenic mouse; hIk-1; immunocomprised; immune system disorder; nervous system disorder;
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                                                                                                                                                                                                                                                                                                                                                                                        Length 537;
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                                                                                                                                                                                                                                                                                                                                                           Score 682.5; DB 1;
Pred. No. 2.2e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                       the corpus striatum
537 AA;
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73.8%;
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Best Local Similarity 73.8'
Matches 127; Conservative
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Matches 127; Conservative
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29-JUL-1994; US-283300.
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

 protein search, using sw model OM protein

(without alignments)
233.179 Million cell updates/sec 6, 1999, 06:55:00 ; Search time 21.23 Seconds November Run on:

US-09-019-348-8 Title:

1126 1 ERDENVLKSEPMGNAEEPEI......VLDRLASNVAKRKSSMPQKF 209 Perfect score: Sequence:

BLOSUM62 Scoring table: 188963 segs, 23686106 residues Searched:

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Aiolos	e Alolos	ide with	1 Ikaros	Ikaros.	Ikaros i	Ikaros 1	s protein	s protein	s zinc f	isofor	č	e Ikaros	Ikaros	Ikaros	Ikaros	ne Ikaros	Ikaros i	ne Ikaros	e Ikaros m	Ikaros i	proteir	s isoform	Ikaros	e Ikaros	Mouse Ikaros mIk-4	Ikaros	s protei	s protei	os protei	cancer	OTK18.	BRCA1-8	zinc fing	268-Zif268 z	zif268-zif26	an SRE-ZBP a	protein. DN		stem cell z	stem ce	ic acid bi	
SUMMARIES	Ω	557	557	969	201	267	960	097	202	W72678	596	297	ᇋ	797	960	707	969	267	960	201	267	960	202	267	96	201	267	960	268	268	268	106	750	218	874	349	439	240	631	175	8163	63	8755	8429
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Zinc finger protei
Amino acid sequenc
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Human Aiolos polypeptide (partial sequence).

Aiolos: transcription activator; immune system; T lymphocyte;

B lymphocyte; leukaemia; lymphoma; asthma; gene therapy;

transgenic animal.
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100.0%; Pred. No. 2.6e-105;
tive 0; Mismatches 0;
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W15575;
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18-0CT-1995; US-005529.
14-MAY-1996; US-017646.
(GEHO ) GEN HOSPITAL CORP.
GEOTGOPOULOS K. MOTGAN BA;
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Matches 209; Conserva
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N-PSDB; T60491.
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Best Local S
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07-JUL-1997 (first entry)
Mouse Aiolos polypeptide.
Aiolos, transcription activator; immune system; T lymphocyte;
B lymphocyte; leukaemia; lymphoma; asthma; gene therapy;
transgenic animal.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
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                                                                                                                                                                                                                                                                                       AA400326 382 bp mRNA EST 16-MAY-1997
2u69b10.rl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743227
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota. Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li (bases I to 382)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,M., Lennon,G., Marra,M., Martin,J., More,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Wahlier,Y., Wyller,T., Waterston,R. and Wilson,R.

WashU-Merck EST Project 1997
On Sep 12, 1995 this sequence version replaced gi:1394077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Bmail: est@wastson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
1.382
                                       340 tgcaactatgcatgccaaagaagaagatgcgctcacggggcatcttaggacacattctgtg 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 83.8; DB 33;
Pred. No. 3.3e~15;
0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:743227"
/clone_llb="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:5930362"
/db_xref="taxon:9606"
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ilarity 55.3%;
Conservative
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78 c
                                                                                                                                                                                                                                                                                                                                         , mRNA sequence
                                                                                                                                                                    gagcacaaggag 471
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Best Local Similarity
Matches 163; Conserv
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92054251
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                                                                                                                                                                                                                                                               RESULT 15
AA400326
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AUTHORS
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Search completed: November 6, 1999, 08:16:51

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us-09-019-348-7.rst

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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"
                                                                                                                         AIS59335 587 bp mRNA EST 13-MAY-1999 tq43h01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2211601 3' similar to SW:ZN16_HUMAN P17020 ZINC FINGER PROTEIN 16 ;, mRNA
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 587) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 aactgcgatgtgtgtgtgtattatcctgcatcagcttcaatgtcttaatggttcataagcga 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 AAGTGTAATGAGTGTGGCCAAGACTTTTGGTCGAAATTCAGCCCTTGTAATTCATAAGGCA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 agccatactggtgaacgcccattccagtgtaatcagtgtggggcatctttactcagaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone-"IMAGE:2211601"
/clone-lib-"NCI_CGAP_Ut1"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host-"DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84.4; DB 48;
Pred. No. 2.5e-15;
0; Mismatches 143;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -400P from Gibco
High quality sequence stop: 402
POLIA-No.
/db_xref="taxon:9606"
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AI559335.1 GI:4509540
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Best Local Similarity 54.2%;
Matches 169; Conservative
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Unpublished (1997)
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                                                                                   RESULT 14
                                                                                                                                                                                                               ACCESSION
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                                                                                                 1 (bases I to 389)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gesel,S., Kucaba,T., Lacy,M., Law, Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwook,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                  WashU HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Exa: 315 266 1810
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:348996
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                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                       Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1404571.
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Pred. No. 1.9e-15;
); Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 347. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:574348"
/clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Mus musculus"
                                                                                                                                                                                                               Waterston, R.
The WashU-HHMI Mouse EST Project
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/dev_stage="4 weeks"
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ilarity 57.1%;
Conservative (
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                                       Mus musculus
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Best Local Similarity
Matches 153; Conserv
                        house mouse.
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KEYWORDS
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Gaps

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Length 587; Indels

2 others

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AA119538 389 bp mRNA EST 17-FEB-1997 mp68a03.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:574348 5',
                                                                                                                                                        Email: est@watson.wustl.edu
Insert Size: 1116
High quality sequence stops: 318 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 taatggttcataagcgaagccatactggtgaacgcccattccagtgtaatcagtgtgggg 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 GAIGCITIACTICIAAAAGAAACCIACTIGAICATCACGAAICCAIACIGGAGAAAAGC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 ttaggacacattctgtggagaaaccctacaaatgtgagttttgtggaaggagttacaagc 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 cttitaagtgtcacctctgcaactatgcatgccaaagaagagatgcgctcacggggcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:35545"
/clone_lib="Soares infant brain INIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.6%; Score 85.2; DB 22;
llarity 57.5%; Pred. No. 1.3e-15;
Conservative 0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="73 days post natal"
                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:408046"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                High quality sequence stop: 318.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 agagaagttcccttgaggagcacaag 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 GTAGTTCTAACTATATTGTGCACCAG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:1677047
      WashU-Merck EST
                        Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AA119538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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AA119538.1
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Matches 153;
      The
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AA119538
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VERSION
                                                                                                                                                                                                                                                                                                                     FEATURES
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High quality sequence stops: 313 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1126 Std Error: 0.00 Seq primer: M13RPl High quality sequence stop: 313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 cttttaagtgtcacctctgcaactatgcatgccaaagaagaggatgcgctcacgggggatc 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      taatggttcataagcgaagccatactggtgaacgcccattccagtgtaatcagtgtgggg 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catcttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaaaaac 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 GATGCTTTACTTCTAAAAGAAACCTACTTGATCATCACCGAATCCATACTGGAGAAAAGC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 ttaggacacattctgtggagaaaccctacaaatgtgagttttgtggaaggagttacaagc 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 AGAGGATACATACTGGGGAGAAACCTTTCAAATGTATGGAATGTGAGAAAGCATTCAGCT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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1 (bases 1 to 431)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 TAATGCGGCATCAGAGAATTCACACTGGGGAGAAACCTTTTGAATGTAATGAGTGTGGGGA 89
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yg47a01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone
IMAGE:35545 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                   /clone_lib="Soares infant brain lNIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.6%; Score 85.2; DB 21;
57.5%; Pred. No. 1.3e-15;
1ive 0; Mismatches 113;
                                                                                                                                                                                                                                                                            /dev_stage="73 days post natal"
                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:404407"
/db_xref="taxon:9606"
/clone="IMAGE:32060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 agagaagttcccttgaggagcacaag 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 GTAGITCIAACIAIATIGIGCACCAG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:777649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 13.6
Best Local Similarity 57.5
Matches 153; Conservative
                                                                                                                                        1. .470
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The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 19712 Medical Center Drive, Rockville, MD 20850 USA 19712 Medical Center Drive, Rockville, MD 20850 USA 19713 Sax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 cttaatggttcataagcgaagccatactggtgaacgcccattccagtgtaatcagtgtgg 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 ACCTIAIACGIGIAAGGAAIGIGGGAAAGCCITCANIGGCAAGICAAAICTCACAGAGCA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 CCTCATTATACATCAGAGAATCCATACTGGAGAAACCTTATGANTGTAAAGGGTGTGG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1995
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1 (bases 1 to 470)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yg12d09.rl Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32060 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 ggcatcttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 accttttaagtgtcacctctgcaactatgcatgccaaagaagagatgcgctcacgggggca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 tottaggacacattotgtggagaaaccotacaaatgtgagttttgtgggaa 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="ArCC (inhost):136466"
/db_xref="taxon:9606"
/clon=lib="Embryo, 9 week"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="embryo, 9 wks"
/note="Vector: pBluescript SK-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 85.6; DB 32,
Pred. No. 8.6e-16;
0; Mismatches 91,
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The WashU-Merck EST Project
Unpublished (1995)
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Best Local Similarity 60.4
Matches 139; Conservative
   Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XhoI
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R17304.1
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AUTHORS
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COMMENT
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KEYWORDS
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1. (bases 1 to 291)

2. Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earl-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S. Jr., Relley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.E., Kocotton, M.C., Saudek, D.M., Shirley, R. Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Liw, W. Hu, J.S., Greene, J.M., Gruber, J., Hustings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J. Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S. M., Dillion, P.J., Farnon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Farnon, M. R., Rosen, C.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                      AA334780 291 bp mRNA EST 21-APR-1997
EST33041 Embryo, 9 week Homo sapiens CDNA 5' end similar to similar
to zinc finger protein HF.10, mRNA sequence.
                                                                                                                       /note-"Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggccaaccagtggaaagatgaactgcgatgtgtgtgtggattatcctgcatcagcttcaatg 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89.4; DB 27; Length 509;
Pred. No. 7.2e-17;
0; Mismatches 41; Indels 0;
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                           /tissue_type="placenta"
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'sex="unknown"
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AA334780.1 GI:1987023
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Best Local Similarity 73.5%;
Matches 114; Conservative
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AA334780
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AA027561/c
                                                                                 BASE COUNT
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High quality sequence stops: 257
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1816 Std Error: 0.00
Seq primer: M13RP1
                                                                 402
                 242 AAACCTTTCAAATGTATGGAATGTGAGAAAGCATTCAGCTGTAGTTCTAACTATTGTG 301
                                                                                                                                                                                                                                                                                                              H83408 355 bp mRNA EST 13-NOV-1995
ys90h12.rl Soares retina N2b5HR Homo sapiens cDNA clone
IMAGE:222119 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Prinates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 355; Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
aacctcctccgccacattaaactgcacacaggggaaaaaccttttaagtgtcacctctgc
                                                                                     aactatgcatgccaaagaagaagatgcgctcacggggcatcttaggacacattctgtggag
                                                                                                                                   aaaccctacaaatgtgagttttgtggaaggagttacaagcagagaagttcccttgaggag
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444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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Unpublished (1995)
On Jan 24, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:3850880"
/db_xref="Exacn:9606"
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/db_rrief="Taxon:9606"
/db_rrief="Taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares retina N2b5HR"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 257.
Location/Qualifiers
1. .355
                                                                                                                                                                                                                                                                                                                                                                                       g1062079
H83408.1 GI:1062079
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H83408
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AA027561 509 bp mRNA EST 21-JAN-1997 milde013.r1 Scares mouse placenta 4NbMPl3.5 14.5 Mus musculus cDNA clone IMAGE:459676 5' similar to gb:L03547 Mouse Ikaros DNA binding protein (MOUSE); mRNA sequence.
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155
Caucasian and total cellular poly(A)+ RNA was extract hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. " 2 others
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                            36 GGCCTGAGGAAACATCATAGAACACACACAGGGGAGAAGCCCTACAAATGTAATCAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 ggggcatcttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaa
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/db_xref="taxon:10090"
/clone="IMAGE:459676"
/clone_lib="Soares mouse placenta 4NbMPl3.5 14.5"
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Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:693622.
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                                                                                                                                                                                                                                                     Score 89.6; DB 24; Length 3
Pred. No. 5.6e-17;
0; Mismatches 89; Indels
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis,
Fax: 314 286 1800
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                                                                                                                                                                                                                                                       14.3%;
61.6%;
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Best Local Similarity 61.69
Matches 143; Conservative
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49 GGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
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R19256.1
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Matches 171;
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
AAB08413 339 bp mRNA EST 19-FEB-1998 oa43h06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1307771 3. similar to TR:000598 000598 HIK1. ;, mRNA sequence.
                                                                                                                                                                                              1 (bases 1 to 339)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1150
Email: Robert Strausbergenth.gov
Iissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 ggccaaccagtggaaagatgaactgcgatgtgtgtggattatcctgcatcagcttcaatg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 GACCTICTAACGGAAAACTAAAGIGIGATATCIGIGGGAICATITGCATCGGGCCCAAIG 110
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                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                            Ph.D., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2153413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.8%; Score 93; DB 38; Length 339; 72.7%; Pred. No. 5.1e-18; Live 0; Mismatches 45; Indels
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1307771"

/clone=11b="WCI_CGAP_GCB1"

/tissue_type="germinal center B cell"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 457 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 295. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ww-bio.llni.gov/bbrp/image/image.html
                                                                                 92877819
AA808413.1 GI:2877819
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AUTHORS
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                                                                ACCESSION
                                                                                             VERSION
KEYWORDS
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@waston.wustl.edu
Insert Size: 1113
High quality sequence stops: 311 Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@linage.llnl.gov) for further information. Insert Length: 1113 Std Error: 0.00 Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 tgcgatgtgtgtgtgtgttatcctgcatcagcttcaatgtcttaatggttcataagcgaagc 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Prinates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 467).

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Klucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
       14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TGTAATGAGTGTGGAAAGGCCTTCAGCGTTAATGGGAAACTAATGCGGCATCAGAGAATT 61
R19256 467 bp mRNA EST 14-APR-199
yg24h05.rl Soares infant brain 1NIB Homo sapiens cDNA clone
IMAGE:33351 5', mRNA sequence.
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55.9%; Pred. No. 4.6e-17;
ive 0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares infant brain lNIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:405698"
/db_xref="taxon:9606"
/clone="IMAGE:33351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 311.
Location/Qualifiers
1. .467
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Best Local Similarity
Matches 155; Conserv
                                                   Waterston, R
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AUTHORS
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                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gaaaaaccttttaagtgtcacctctgcaactatgcatgccaaagaagaagatgcgctcacg 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 tgtggggcatcttttactcagaaaggtaacctcctccgccacattaaactgcacacaggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 609;
                                            MGI:673927
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity on wrong strand
Possible reversed clone: Stop Amersham
High quality sequence stop: 423.
Location/Qualifiers
1. .609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
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Pred. No. 3e-44;
0; Mismatches
                                                                                                                                                                           /clone_lib=Scares_2NbMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4" weeks"
/lab_host="DH10B"
           Email: mouseest@watson.wustl.edu
                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1282127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 GGACACCTIAGGACACATICIG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 gggcatcttaggacacattctg 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.6%;
Best Local Similarity 87.8%;
Matches 230; Conservative
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Eutheria; Rodentia;
1 (bases 1 to 557)
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Mus musculus
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Best Local Similarity
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Law, Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Théising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 ccagtggaaagatgaactgcgatgtgtgtggattatcctgcatcagcttcaatgtcttaa 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 CCTTTACCCAGAAAGGCAACCTCCTGCGGCACATCAAGCTGCACTCGGGTGAGAAGCCCT 27
                                                                                                                               The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 17, 1998 this sequence version replaced gi:1900564.
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                                                                                                                                                                                                                                                                                                          444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:459676"
/clone_lib="Soares mouse |
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seg primer: -40RP from Gibco
High quality sequence stop: 417.
Location/Qualifiers
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/map="21"
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Query Match Best Local

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Mus musculus
Eukaryota, Mactazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 609)
Marta, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Agera, M., Teo, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA920812 609 bp mRNA EST 20-APR-1998 vx86f12.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1282127 5' similar to TR:008900 008900 AIOLOS ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 tectgeateagetteaatgtettaatggtteataagegaageeataetggtgaaegeeca 240
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On Sep 12, 1996 this sequence version replaced 91:1407236
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                          1 others
                                                                                                                                                                                                                                                                                                                                                                                tch 29.5%; Score 185; DB 48; Length 5 al Similarity 80.9%; Pred. No. 6.5e-46; 228; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1264352"
/clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
                                                      /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
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AA920812.1 GI:3067591
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Matches 228)
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1 (bases 1 to 501)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                         ccttacagctattcaagagaatataatgaatatgaaaacattaagttggagagacatgtt 120
                                                                                                                                                                                                                                                                   AI550402 501 bp mRNA EST 23-MAR-1999 vx13e05.x1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1264352 similar to TR:O08900 O08900 AIOLOS ;, mRNA sequence.
                                                                                                               1 gaaagagatgagaatgttttaaagtcagaacccatgggaaatgcagaagacctgaaatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
On Jun 22, 1998 this sequence version replaced gi:3246999
                                                                          ñ
                                     Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found High quality sequence stop: 381.

Location/Qualifiers
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone was previously sequenced on the 5' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                     DB 48;
                                                                        45;
                                                    Pred. No. 1.7e-62;
                                   Score 239.6;

    .501
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĀI550402.1 GI:4482765
                                 38.2%;
Similarity 85.3%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1550402
                                                                        Matches 279;
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DEFINITION

ACCESSION

RESULT AIS50402

301

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ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

TITLE JOURNAL

COMMENT

source

FEATURES

399

459

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AI549961.1 GI:4482324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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JOURNAL
                                                                              516
                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                          RESULT
AI549961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 577)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctctgcaactatgcatgccaaagaagagtgcgctcacggggcatc-ttaggacacattc 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgtggagaaaccctacaaatgtgagttttgtggaaggagttacaagcagagaagttccct 455
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                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jun 27, 1996 this sequence version replaced gi:1184736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.3%; Score 303.4; DB 39; Length 577; ilarity 86.2%; Pred. No. 7.3e-82; Conservative 0; Mismatches 55; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 Fr from Amersham High quality sequence stop: 270.
                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / S77 / Corganism="Mus musculus" / Strain="CSPBL/G" / GLarin="CSPBL/G" / Clone="IMAGE:1282191" / Clone_lib="Soares ZNbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
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hes 356;
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Matches
                                       ORGANISM
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ORIGIN
                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                             REFERENCE
AUTHORS
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KEYWORDS
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" (bases I to 546)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R., And Wilson, R., The Washullon, R., Morann, R., Waterston, R. and Wilson, R. The Washullon Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
High quality sequence stop: 460.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         AIS49961 546 bp mRNA EST 23-MAR-1999 vx02e08.x1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1263302 3' similar to TR:008900 008900 AIOLOS ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
aagtgcggaggcaagacacatcaaagcagagatgggaagtgaaagagctctcgtactgga 575
                                                                                                                                               278 AAGTGTGGAGGCAAGACACATCAAAGCCGAGATGGGAAGTGAGAGAGCTCTCGTCGA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Jun 5, 1998 this sequence version replaced gi:3189635
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentía; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="InAGE:1263302"
/clone=lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .546 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
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4.5
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 1998
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6, 1999, 08:16:48; Search time 437.25 Seconds
(without alignments)
2833.050 Million cell updates/sec gaaagagatgagaatgtttt.......ctcaatgcctcagaaattca residues sw model 2546578 seqs, 986266752 using en_est1::*
en_est2::*
en_est3::*
en_est5::*
en_est5::*
en_est6:*
en_est6:*
en_est10:*
en_est10:* US-09-019-348-7 628 nucleic search, IDENTITY_NUC November EST:* Title: Perfect score: Sequence: Scoring table: •• OM nucleic Searched: Database Run on:

AA863970 vx87d08.r AI5549561 vx02e08.x AA520402 vx13e05.x AA9208413 vx86f12.r AA8028413 vx86f12.r AA802564 m106e03.r AA34780 EST39041.r1 AA34780 EST3904.r R1734 y912d09.r1 R1734 y912d09.r1 R1734 y912d09.r1 R1734 y912d09.r1 R2594 y947a01.r1 AA19538 mp68a03.r AA10256 mp68a03.r AA10256 mp68a03.r AA10257 y175b08.r1 AA10551 y175b08.r1 AA10555 EST234821 A1042864 homo sapi AA44430 EST191190 A104264 homo sapi AA44430 EST191190 A104264 homo sapi AA44430 EST191190 A104264 homo sapi AA44313 qh88f01.x AA622972 aE78h12.s AA772346 a143c08.s AA772346 a143c08.s AA772346 a143c08.s AA772346 a143c08.s AA77241 aA8881 a13c08.s AA5772 aa22e04.r AA628881 a430a12.s Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES AA863970 H **Რ**4444m020m02044m044d4m5m44mm44mm60m60m em_est23:* em_est24:* em_est25:* em_est26:* ΩB em_est22:* % Query Match Length D 5555... 303.4 239.6 185 179.6 125 Score Result No. 000

AA113952 zm81c11.r A1128612 qa62a10.s A1311718 qo92f08.x T63663 yc23a03.r1

gb_est19:*
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gb_est24:*
gb_est25:*
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gb_est27:*
gb_est27:*
gb_est28:*

gb_est31:*
gb_est32:*
em_est20:*
em_est21:*

gb_est30

AA548358 nk41a05.3 AA624117 vq75907.5 R98364 HH2105F Hum R98368 HH2115F Hum AA917951 ol68911.5 W27601 35a3 Human

AA171117 AI406535 HSM009139 HSM007817 AA848430

AA628972 AA772346 AA789218

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em_est17...
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gb_est2...
gb_est4...
gb_est5...
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gb_est11...

em_est14:* em_est15:* em_est16:*

em_est13

AA814418 AA455712 AA628881 W28371

AA972741 W19169

H05551 AI648952

ALIGNMENTS

LEST 11-MAR-1998 vx87d08.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1282191 5' similar to TR:008900 008900 AIOLOS;, mRNA sequence. AA863970 92956449 AA863970.1 GI:295642 LOCUS RESULT 1 AA863970/c ACCESSION NID VERSION

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ZUCHAIN OSA ZUCHAIN OSA ZUCHAIN OSA ZUCHAIN OSA ZUCHAIN TYPE: Diskette COMPUTER: Diskette COMPUTER: TBM Compatible OPERATING SYSTEM: DOS SOTTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/933,750C FILING DATE: September 23, 1997 CLASSIFICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER: ELING DATE:
                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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                   COUNTRY:
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Sequence 53, Application US/08933750C

Patent No. 5932442

GENERAL INFORMATION:

APPLICANT: Lal, Preetl

APPLICANT: Bandman, Jennifer L.

APPLICANT: Shah, Purvi

APPLICANT: Shah, Purvi

APPLICANT: Au Young, Janice

APPLICANT: Young, Janice

APPLICANT: Corley, Neil C.

TILLE OF INVENTION: HUMAN REGULATORY MOLECULES

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106.6; DB 5;
Pred. No. 1.5e-25;
0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 02-MAY 94
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MGP-027PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-7401
TELEPHONE CRARACTERISTICS:
SEQUENCE CHARACTERISTICS:
               SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.1%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
PCT-US95-09345-7
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                                                                                                                                                                                                                                      163 tgcgatgtgtgtgtgtatcctgcatcagcttcaatgtcttaatggttcataagcgaagc 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 aacctcctccgccacattaaactgcacagagggaaaaaccttttaagtgtcacctctgc 342
                                                                                                                                 Length 2031;
                                                                                                                              Ouery Match 11.6%; Score 72.8; DB 4; Length 2 Best Local Similarity 53.5%; Pred. No. 2.6e-14; Matches 152; Conservative 0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 aaaccctacaaatgtgagttttgtggaaggagttacaagcagag 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 6, 1999, 06:57:40
Job time: 141 sec
LIBRARY: HMCINOT01;
CLONE: 9337
US-08-933-750C-53
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229 ggigaacgcccattccagigaatcagigigggcatcittactcagaaaggtaaccic 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%; Score 106.6; DB 3; Length 1004; 75.1%; Pred. No. 1.5e-25; tive 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application PC/TUS9509345
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESSEE: LAHIYDE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: AscII (text)
SOFTWARE: AscII (text)
APPLICATION DATA:
APPLICATION NUMBER: US (08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (08/121,438
FILING DATE: US -MAY-1994
PRIOR APPLICATION NUMBER: US (08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION NUMBER: US (07/946,233
FILING DATE: 14-SEP-1993
ATTORNEY AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: 35,695
REFERENCE/DOCKET NUMBER: 35,695
REFERENCE/DOCKET NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1004 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.1
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
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; LOCATION:
US-08-465-590-8
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PCT-US95-09345-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 GGTGAACGGCCTTTCCAGTGCAACCAGTCTGGGGCCTCCTTTACCCAGAAAGGCAACCTC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Sequence 8, Application US/08465590

Sequence 8, Application US/08465590

Patent No. 584770

PAPLICANT: Georgopoulos, Katia A.

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 164

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1170;
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Pred. No. 7.6e-26;
0; Mismatches 39;
                                                                                                                                                                                                                                 PRIORING APPLICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-JULY 94
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
PROOR APPLICATION DATA: 4
PRIOR APPLICATION DATA: 4
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: MYETS, PAUL L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MGP-027PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFANO: (617)227-7400
TELEFANO: (617)227-7401
TELEFANO: (617)227-7501
TELEFANO: (617)227-7501
TELEFANO: (617)227-7501
                                                      COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AscII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUCETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.1%;
Best Local Similarity 77.1%;
Matches 131; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 1170 base pairs
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STRANDEDNESS: single
  MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA FEATURE:
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; LOCATION: 1..1
PCT-US95-09345-5
STATE: M
COUNTRY:
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289 ctccgccacattaaactgcacacaggggaaaaacttttaagtgtcacctctgcaactat 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.1%; Score 107.6; DB 3; Length 1 Best Local Similarity 77.1%; Pred. No. 7.6e-26; Matches 131; Conservative 0; Mismatches 39; Indels
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PCT-US95-09345-5
SQUENCE 5. Application PC/TUS9509345
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
ITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-00N-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATORNEY AGENT INFORMATION:
RME: Myers, Paul L.
RECISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MFG-006C2DV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: (617)227-7400
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUCETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                MASSACHUCETIS: USA
               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..1170
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                                                                                                                                                                                            COUNTRY: U:
ZIP: 02109
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; LOCATION:
US-08-465-590-6
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Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: GEOTGOPOULOS, Katia A.
TITLE OF INVENTION: IKAROS: A T.CELL PATHWAY REGULATORY GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-JULY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1992
ATTONNEY AGENT INPORMATION:
NAME: MYSETS, PBUL L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: 35,695
REFEREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578 GGACGCACTCCGGAGACAA 596
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LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
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; LOCATION: 1..1296
PCT-US95-09345-3
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                            Query Match 27.1%; Score 170; DB 5; Length 1788; Best Local Similarity 67.1%; Pred. No. 3.5e-46; Matches 283; Conservative 0; Mismatches 115; Indels. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT GEOTOPOULOS, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUCETTS
COUNTRY: USA
NAME: Myers, Paul L.

REGIGSTRATION NUMBER: 35,695

REFERENCE/DOCKET NUMBER: MGP-027PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CECUT 9
INS-08-465-590-4
Sequence 4, Application US/08465590
Patent No. 5824770
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 223..1515
PCT-US95-09345-1
                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
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|802 TT 803
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326 ttaagtgtcacctctgcaactatgcatgccaaagaagagatgcgctcacggggcatctta 385
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Sequence 3, Application PC/TUS9509345
GENERAL INFORMATION:
SAPPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 148.6; DB 3;
Pred. No. 3e-39;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                OURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: US-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: US-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGIGTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617)227-591
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 ggacacattctgtggagaa 404
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Best Local Similarity 73.4%;
Matches 190; Conservative
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Best Local Similarity
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us-09-019-348-7.rni

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Gaps

24;

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ggigaacgcccattccagigtaatcagigiggggcatcittacicagaaaggiaaccic 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 GGTGAACGGCCTTTCCAGTGCAACCAGTCTGGGGCCTCCTTTACCCAGAAAGGCAACCTC 441
                                                                                                                                                                                                                                                                                                                                                                                                                        622 GAGCGATGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCGTGTGCCCAGTCATTAAG 681
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                                                                                                                                                                                         gagogotgocotacatttottoagagoactgaco----cagogogacactgoaagtgog
                      Length 1788;
                  Query Match 27.1%; Score 170; DB 5; Length 178 Best Local Similarity 67.1%; Pred. No. 3.5e-46; Matches 283; Conservative 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9509345
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IRAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
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ZURINI 1 02-0

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: ASII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-WAY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
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APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-UULY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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PCT-US95-09345-1
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                                                                                                                                                                  442 CIGCGGCACATCAAGCIGCACICGGGIGAGAAGCCCIICAAAIGCCAICIIIGCAACIAI 501
                                                                                                                                                                                                                                                                                             gcatgccaaagaagagatgcgctcacggggcatcttaggacacattctgtggagaaaccc 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                         gagegetgeegtacattetteagageactgace----eaggggaeactgeaagtgeg
                                                                                                             24;
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COMPUTER READABLE FORM:
MEDIUM TYEE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCLI
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
                                                                     Score 170; DB 3; Length 1788; Pred. No. 3.5e-46; 0; Mismatches 115; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9308743
GENERAL INFORMATION:
APPLICANT:
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illarity 67.1%;
Conservative (
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; LOCATION: 223..1515
PCT-US93-08743-2
; LOCATION: 223..1515
US-08-465-590-2
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                                                                                        Best Local Sim
Matches 283;
                                                                     Query Match
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326 ttaagtgtcacctctgcaactatgcatgccaaagaagagatgcgctcacggggcatctta 385
                                             740 TCAAATGCCATCTTTGCAACTATGCCTGCCGCGGAGGGACGCCCTCACCGGCCACCTGA 799
                                                                                        386 ggacacattctgtggagaaaccctacaaatgtgagttttgtggaaggagttacaagcaga 445
                                                                                                                                      800 GGACGCACTCCGTTGGTAAGCCTCACAAATGTGGATATTGTGGCCGGAGCTATAAACAGC 859
                                                                                                                                                                                                             920 CGGCCGTGTGCCCCAGTCATTAAGGAAGAACTAACCACAACGAGATGGCAGAAGACCTGT 979
                                                                                                                                                                                                                                                                                                                                                                  542 cagagatgggaagtgaaagagetetegtaetggacagattagcaagcaatgtggcaaaae 601
                                                                                                                                                                                   446 gaagttcccttgaggagcacaaggagcgctgccgtacatttcttcagagcactgacc---
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TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                            503 ---caggggacactgcaagtgcggaggcaagacacatcaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: ITEL TOPPY ALLSA COMPUTER: TEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Ascil (text)

CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/465,590 FILING DATE: 05-UNN-1995 FRIOR APPLICATION NUMBER: US 08/238,212 FILING DATE: 02-MAY-1994 PRIOR APPLICATION NUMBER: US 08/121,438 FILING DATE: 14-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/946,233 FILING DATE: 14-SEP-1993 ATTORNEY/AGENT INFORMATION: NAME: Myers, Paul L. REGISTRATION NUMBER: 35,695 REFERENCE/DOCKET NUMBER: 35,695 REFERENCE/DOCKET NUMBER: Myer-006C2DV TELECOMMUTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1040 GTAAGAGCTCTATGCCTCAGAAATT 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                           602 gaaaaagctcaatgcctcagaaatt 626
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US-08-465-590-2
; Sequence 2, Application US/08465590
; Patent No. 5824770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MASSACHUCETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 regricacaaaagaagicaracregreaacegccrirccagrecaaccagreregegccr 679
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                                                                                                         Sequence 4, Application PC/TUS9509345
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 209.8; DB 5;
Pred. No. 3.4e-59;
0; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MGP-027PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-UULY-94
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAX-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
                                                                                                                                                                                                                                                 ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
1040 GTAAGAGCTCTATGCCTCAGAAATT 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.4%;
Best Local Similarity 67.1%;
Matches 339; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                           STREET: 60 SIALE CITY: BOSTON STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 223..1776
PCT-US95-09345-4
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                                                                   RESULT 5
PCT-US95-09345-4
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NAME/KEY: CDS

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ggacacattctgtggagaaaccctacaaatgtgagttttgtgggaaggagttacaagcaga 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttaagtgtcacctctgcaactatgcatgccaaagaagagatgcgctcacgggggcatctta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               860 GAAGCTCTTTAGAGGAGCATAAAGAGCGATGCCACAACTACTTGGAAAGCATGGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 CGGGCGTGTGCCCCAGTCATTAAGGAAGAACTAACCACAACGAGAGATGGCAGAAGACCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 209.8; DB 3;
Pred. No. 3.4e-59;
0; Mismatches 142;
                          CURRENT ABOLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: US 08/121,438
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: US 08/121,438
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
PRIOR APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEX/AGENT INFORMATION:
NAME: MYGEN FAUL L.
RECIETRATION NUMBER: MG-006C2DV
TELEOVAMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7401
INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
LUMOTH: 2049 DASE PAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.4%;
Best Local Similarity 67.1%;
Matches 339; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
223..1776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-08-465-590-5
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Patent No. 5824770
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 164
CORRESSONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STREET, Suite 510
CITY: BOSTON
                                                                                                                                                                                                                                                                          Length 1386;
                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 1.9e-61;
0; Mismatches 136;
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                                                                                                                                                                                                                                                                          Query Match 34.5%;
Best Local Similarity 67.9%;
Matches 345; Conservative
               TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
I.ENGTH: 1386 base pairs
(617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                       nucleic acid
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COUNTRY: USA
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                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                             linear
                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                   ; LOCATION:
PCT-US95-09345-2
                                                                                                                             TOPOLOGY:
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                                     ttaagtgtcacctctgcaactatgcatgccaaagaagaatgcgctcacggggcatctta 385
                                                                                                                                                                         755 CGGCCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGACC 814
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PCT-US95-09345-2
Sequence 2, Application PC/TUS9509345
Sequence 2, Application PC/TUS9509345
Sequence 2, Application PC/TUS9509345
FITHER PRINCANT: Georgopoulos, Katia A,
TITHE OF INVENTION: TARNOS TRANSCENIC CELLS AND ANIMALS
TUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-ULX'-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAX'-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US95/09345 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MGP-027PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             599 aacgaaaaagctcaatgcctcagaaatt 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: MYETS, Paul L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII (text
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                133 TGGTTCACAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCT
                                                                  cttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaaaaacctt
                                                                                                                                     ttaagtgtcacctctgcaactatgcatgccaaagaagagaggcgtcacgggggcatctta
                                                                                                                                                           353 TCAAATGCCACCTCTGCAACTACGCCTGCCGCGGAGGGACGCCCTCACTGGCCACCTGA
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                                                                                      CATTCACCCAGAAGGGCAACCTGCGCACATCAAGCTGCATTCCGGGGGAGAAGCCCT
                                                                                                                                                                                                                                                                                                                                                                              533 CGGGCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION NUMBER: PCT/US93/08743
FILING DATE: 14-SEP-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7401
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1611 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aacgaaaaagctcaatgcctcagaaatt 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application PC/TUS9308743 GENERAL INFORMATION:
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Best Local Similarity
Matches 345; Conserv
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PCT-US93-08743-3
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PCT-US93-08743-3
206
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                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-08-465-590-3
i Sequence 3, Application US/08465590
i Patent No. 5824770
i GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
ITLE OF INVENTION:
INUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
        Sequence 2
Sequence 3
Sequence 1
Sequence 1
Sequence 3
Sequence 3
Sequence 3
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PCT-US96-03940-27
PCT-US96-03940-28
US-08-224-482-3
US-08-616-857-1
US-08-909-965C-3
US-08-040-5548-31
US-08-466-344-31
US-08-224-482-5
                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MFG-006C2DV TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHWARE: Ascil (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-UN-1995
FILING DATE: 02-WAY-1994
PRIOR APPLICATION NUMBER: US 08/238,212
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
APPLICATION NUMBER: US 07/946,233
REGISTRATION NUMBER: 35,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: BOSTON
STATE: MASSACHUCETTS
CONTORY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 1386 base pairs
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STRANDEDNESS: double
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; LOCATION:
US-08-465-590-3
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1475.260 Million cell updates/sec
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Sequence 6, A
Sequence 10,
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1: /cgn2_c/ptodata/lina/5A_COMB.seq:*

2: /cgn2_f/ptodata/lina/5E_COMB.seq:*

3: /cgn2_f/ptodata/l/ina/5C_COMB.seq:*

4: /cgn2_f/ptodata/l/ina/5D_COMB.seq:*

5: /cgn2_f/ptodata/l/ina/FOLOMB.seq:*

6: /cgn2_f/ptodata/l/ina/Pockfiles1.seq:*
                              GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-465-590-2
PCT-US93-08743-2
PCT-US93-09345-1
US-08-465-590-4
US-08-465-590-6
US-08-465-590-6
US-08-465-590-6
US-08-465-590-8
US-08-933-750C-63
US-08-933-750C-63
US-08-933-750C-65
US-08-94-96-1
US-08-94-96-1
US-08-94-96-1
US-08-46-344-14
US-08-466-344-14
US-08-466-344-14
US-08-466-344-14
US-08-466-344-14
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PCT-US96-03940-10
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US-08-465-590-5
PCT-US95-09345-4
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PCT-US96-03940-4
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628
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contained the 1788 bp sequence. A 300 bp 3'-terminal segment of this was used to identify 4 other Ikanos isoforms (see 442807-10). Different isoforms arise by differential splicing of Ikaros gene transcripts. Isoform mIk-2 lacks exon 3. It is expressed in embryonic liver, thymns and brain, but only in thymns and splaen after birth. The Ikaros gene is located at the proximal arm of murine chromosome 11. Ikaros proteins are suggested to play a role as a genetic switch regulating entry into the T cell lineage. The murine and human (see V42806, V42811 and V4280) Ikaros sequences are very similar. The invention provides Ikaros nucleic acids, cetors and host cells expressing Ikaros proteins. These are used to treat T and B cell diseases (e.g. timmune deficiencies caused by drugs, radiation or cancers), to control expression of heterologous cross placed under control of an Ikaros responsive element, to modulate cell division, amplification or differentiation, especially the namatopoietic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences. The same effect can be achieved with Ikaros-binding oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggtgaacgcccattccagtgtaatcagtgtggggcatcttttactcagaaaggtaacctc 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-1996 (first entry)
Murine Ikaros cDNA mIk-3.
Murine Ikaros cDNA mik-3.
Ikaros; transgene; transgenic animal; transgenic mouse; mIk-3; immunocomprised; immune system disorder; nervous system disorder; animal model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                               acquiring the above
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27.1%; Score 170; DB 1; Length 1788;
Best Local Similarity 67.1%; Pred. No. 3.8e-45;
Matches 283; Conservative 0; Mismatches 115; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                  370 T;
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G
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                                                                                                                                                                                                                                                                                                                                                                             structure, can be used to assess risk of
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Mus musculus

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Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine referets of treatment for immune and nervous system disorders. Disclosure: Page 63-64; 102pp; English.

CDNA clones (716059 and 716061-64) encode different isoforms, mix-3, mix-1, mix-4 and mix-5 (R92014 and R92016-19).

C mix-2, mix-3, mix-1, mix-4 and mix-5 (R92014 and R92016-19).

C respectively), of the mouse Ikaros protein, a master regulator of hematopoietic differentiation. They were isolated from a mature controlline E-14 cDNA library. The isoforms arise by differential splicing of the Ikaros genomic locus. All include exons E1/2 and E7, but have different combinations of exons E3-E6 encoding a zinc finger domain. Transgenic animals, pref. mice, having a mutated Ikaros transgene, esp. a mutation that all, iss the DNA binding domain of the Ikaros protein, are used as models to determine the effects of treatments for immune or nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 CCTTTACCCAGAAAGGCAACCTCCTGCGGCACATCAAGCTGCACTCGGGTGAGAGCCCT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttaagtgtcacctctgcaactatgcatgccaaagaagagatgcgctcacggggcatctta 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 148.6; DB 1; Length 1296;
Pred. No. 2.7e-38;
0; Mismatches 69; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 C;
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ilarity 73.4%;
Conservative (
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                               28-JUL-1995; U09345.
29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1296 BP;
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Best Local Similarity
Matches 190; Conserv
                                                                                          Georgopoulos K;
WPI; 96-129389/13.
                                                                                                                              P-PSDB; R92016
               .5-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trains pluy; peptidets) - useful for treating disorders of immune system or corpus striatum

Disclosure; Column 51-56; 111pp; English.

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFRB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFRB element or an Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikaros isoform to any of a delta A element, an NFRB competitively inhibits protein-protein interactions of transcriptional complexes competitively inhibits protein-protein interactions of transcriptional complexes that they stimulate gene transcription under the control of delta A elements, NFRB elements and/or Ikaros-binding oligonucleotides, competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements, NFRB elements and/or Ikaros-binding oligonucleotides, competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements, NFRB elements and/or Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-responsive elements and/or iharos-responsive elements and/or iharos-re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence encodes a specifically claimed mouse Ikaros protein. 437 A; 486 C; 495 G; 370 T;
                                                                                                                                                                                                          Murine Ikaros encoding cDNA mik-2.
CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
differentiation marker; immune system; corpus striatum; AIDS;
tacaaatgtgagttttgtggaaggagttacaagcagagagttcccttgaggagcacaag 468
                  gagogotgocogtacatttcttcagagoactgaco----caggggacactgcaagtgog 522
                                                                                                                                          gaggcaagacacatcaaag----------cagagatgggaagtgaaagagct
                                                                                                                                                                GAGCGATGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCGTGTGCCCAGTCATTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ikaros poly:peptide(s) - useful for treating disorders of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223. .1518
/*tag=
/product= "mik-2"
/transl_except= (pos:385. .387,aa:Gln)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 1788 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-1994; US-238212.
14-SEP-1992; US-946233.
14-SEP-1999; US-121438.
05-UUN-1995; US-465590.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease; ss.
Mus sp. Location,
Key 223. .151
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WPI; 98-582621/49.
P-PSDB; W72671.
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802 TT 803
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WPI: 98-37829/33.

R WPI: 98-37829/33.

P-PSDB: 470963.

P-PSDB: 470963.

T differentiation of lymphocytes - existing in several isoforms, and differentiation of lymphocytes - existing in several isoforms, and a control cell differentiation.

Claim 7: Page 68-70: 158pp: English.

Claim 7: Page 68-
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                                                                                          Gaps
                                                                                                                                                                           ggtgaacgcccattccagtgtaatcagtgtggggcatcttttactcagaaaggtaacctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 GGTGAACGGCCTTTCCAGTGCAACCAGTCTGGGGCCTCCTTTACCCAGAAAGGCAACCTC
                                                                                                                                                                                                                                                                                                                                      ctccgccacattaaactgcacacaggggaaaaaccttttaagtgtcacctctgcaactat
                                                                                                                                                                                                                                                                                                                                                                                     409 tacaaatgtgagttttgtggaaggagttacaagcagagaagttcccttgaggagcacaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562 CACAAATGTGGATATTGTGGCCGGAGCTATAAACAGCGAAGCTCTTTAGAGGAGCATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaggcaagacacatcaaag--------gagagatgaagtgaaagagct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        682 GAAGAAACTAACCACAACGAGATGGCAGAAGACCTGTGCAAGATAGGAGCAGAGAGGTCC
                                                                                     24;
        Length 1788
    Score 170; DB 1; Length 178
Pred. No. 3.8e-45;
0; Mismatches 115; Indels
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Mouse Ikaros isoform mik-2 cDNA.
Haros mik-2; transcription factor; mouse; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; ss.
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    27.1%;
67.1%;
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Query Match 27.1
Best Local Similarity 67.1
Matches 283; Conservative
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05-SEP-1996; US-711417.
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11-JAN-1999
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Mus musculus
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TT 803
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T16059
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                                                                                    289 ctccgccacattaaactgcacacaggggaaaaaccttttaagtgtcacctctgcaactat 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggtgaacgcccattccagtgtaatcagtgtggggcatcttttactcagaaaggtaacctc 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                            T-cell pathway regulatory gene, Ikaros - encodes family of unique zinc finger proteins, useful for treating immune system disorders claim 13; page 41-43; 112pp; English.

The Ikaros gene encodes a zinc finger protein which can be used in therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is a fish for an immune disorder. It is of particular use in treating a disorder of the corpus striatum.

Sequence 1788 BP; 437 A; 486 C; 495 G; 370 T;
                                                                                                                                                                                    21-07-1994 (first entry)
Murine Ikaros gene.
Ikaros; zinc finger; protein; immune disorder; therapy; treatment; corpus striatum; regulatory gene; ss.
Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gaagttcccttgaggagcacaaggagcgctgccgtacatttcttcagagcactgacc---
                                                   920 CGGGCGTGTGCCCCAGTCATTAAGGAAGAACTAACCACAACGAGAGGCAGAAGACCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.1%; Score 170; DB 1; Length 1788; ilarity 67.1%; Pred. No. 3.8e-45; Conservative 0; Mismatches 115; Indels 2.
                                                                                                                                                                                                                                                                                               /transl_except= GAA encodes Glutamine
                                                                                                                                                                                                                                                                   /product= Ikaros protein
385. .387
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                   gaaaaagctcaatgcctcagaaatt 626
                                                                                                                                                                         BP.
                                                                                                                                                                       Q44979 standard; cDNA; 1788
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14-SEP-1993; UO8743.
14-SEP-1992; US-946233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query'Match
Best Local Similarity
Matches 283; Conserv
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WPI; 94-118387/14.
                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R46963
                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                      WO9406814-A
                                                                                                                                                                                  044979;
                                                                                                                                                      RESULT 11
Q44979
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Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders. Disclosure: Fig 1: 102pp; English.

CDNA clones (T16059 and T16061-64) encode different isoforms, mix-1, mix-4 and mix-5 (R92014 and R92016-19, caspectively), of the mouse Ikaros protein, a master regulator of hematopoietic differentiation. They were isolated from a mature T-cell in E-14 cDNA library. The isoforms arise by differential splicing of the Ikaros genomic locus. All include exons E1/2 and E7, but have different combinations of exons E3-E6 encoding a zinc finger domain. Transgenic annuals, pref. mice, having a mutated likaros transgene, esp.

a mutation that alters the DNA binding domain of the Ikaros protein, a mutation that alters the DNA binding domain of the Ikaros protein, a models to determine the effects of treatments for immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcatgccaaagaagagatgcgctcacggggcatcttaggacacattctgtggagaaaccc 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctccgccacattaaactgcacacaggggaaaaaccttttaagtgtcacctctgcaactat 348
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                                                                                                                                                                                                                                    622 GAGCGATGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCGTGTGCCCAGTCATTAAG
                                                                                                                                                                             ---caggggacactgcaagtgcg
                                                                                                                       ----cagagatgggaagtgaaagagct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine Ikaros cDNA mIk-2.
Ikaros; transgene; transgenic animal; transgenic mouse; mIk-2;
immunocomprised; immune system disorder; nervous system disorder;
animal model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_except= pos:385. .388:_aa:Gln
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gagcgctgccgtacatttcttcagagcactgacc-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            486 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
233. .1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system disorders.
1788 BP; 437 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; cDNA; 1788
                                                                                                                       gaggcaagacacatcaaag---.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-1995; U09345.
29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 283; Conservative
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WPI; 96-129389/13.
P-PSDB; R92014.
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New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and to control cell differentiation

First st page 75-77; 158pp; English.

Claim 7; Page 75-77; 158pp; English.

Codes for a 518-amino acid 2inc finage protein (see W12805) as mix-1 contains all 7 content and fortified. These arise by differential all 7 contents and the postnatal spleen. The Ixaros gene is not attained at the proximal arm of murine chromosome 11. Ixaros proteins are suggested to play a role as a genetic switch are unded to active and human (see V42806, V42811 and V42840) Ixaros sequences are very similar.

The invention provides Ixaros nucleic acids, vectors and host cells cancers), to control expression of heterologous genes placed under control of an Ixaros responsive element, to treat nervous system diseases (e.g. immune deficiencies caused by drugs, radiation or cancers), to control expression of heterologous genes placed under control of an Ixaros responsive element, to treat nervous system cancers), to control expression of heterologous genes placed control amplification or differentiation, especially in haematopoletic can be achieved with Ixaros sequences. The same effect can be achieved with Ixaros gene, or its all and achieved with its are antagonistic of these sequences can be achieved by achieved by achieved to see the expression of the same effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 ccagtggaaagatgaactgcgatgtgtgtggattatcctgcatcagcttcaatgtcttaa 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggacacattctgtggagaaaccctacaaatgtgagttttgtgggaagtacaagcaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 5.7e-58;
0; Mismatches 142;
  /*tag= e
/number= Ex5
934 1076
/*tag= f
                                                                                         /number= Ex6
                                                                                                              1077. .1779
                                                                                                                                                                                                                                               05-SEP-1996; US-711417.
(GEHO ) GEN HOSPITAL CORP.
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/number= E
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Matches 339; Conservative
                                                                                                                                                                                                        05-MAR-1998.
02-JAN-1997; 194256
                                                                                                                                                                                                                                                                                           Georgopoulos K;
WPI; 98-378292/33.
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competitively inhibit Ikaros binding to Ikaros-responsive elements and/or inhibit protein-repotein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence encodes a specifically claimed mouse Ikaros protein. 531 C; 574 G; 430 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccagtggaaagatgaactgcgatgtgtgtggattatcctgcatcagcttcaatgtcttaa 205
                                                                                                                                                                                                                                                                                                                                    560 CTAACGGAAAACTAAAGTGTGATATCTGTGGGATCGTTTGCATCGGCCCAATGTGCTCA 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaaaaactt 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 860 GAAGCTCTTTAGAGGAGCATAAAGAGCGATGCCACAACTACTTGGAAAGCATGGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---caggggacactgcaagtgcggaggcaagacacatcaaag------
                                                                                                                                                                                                   Score 209.8; DB 1; Length 2049;
Pred. No. 5.7e-58;
0; Mismatches 142; Indels 24;
                                                                                                                                                                                                 Length 2049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Ikaros isoform mIk-1 cDNA.
Ikaros; mIK-1; transcription factor; mouse; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1040 GTAAGAGCTCTATGCCTCAGAAATT 1064
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/*tag= a
223. .384
/*tag= b
/number= Ex1/2
385. .643
/*tag= c
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Best Local Similarity 67.1%;
Matches 339; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             811. 933
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System of colpum stilatum

Disclosure; Column 61-66; 111pp; English.

The present invention describes a purified peptide having at least one
of the following properties: (a) it stimulates transcription of a DNA
sequence under the control of a delta A element, an NFKB element or an
Ikaros binding oligonuclectide consensus sequence; (b) it binds to any of
a delta A element, an NFKB element or an Ikaros binding oligonuclectide
consensus sequence; (c) it competitively inhibits the binding of a
consensus sequence; (d) it competitively inhibits the binding of a
competitively inhibits Ikaros binding to Ikaros responsive element; or
(e) it inhibits Ikaros binding to Ikaros responsive elements; or
(e) it inhibits protein protein interactions of transcriptional complexes
(formed with naturally occurring Ikaros isoforms. The proteins, provided
that they stimulate gene transcription under the control of delta A
ce elements, NFKB elements and/or Ikaros-binding oligonucleotides,
celements, NFKB elements and/or Ikaros-binding oligonucleotides,
competitively inhibit binding of naturally occurring Ikaros isoforms to
delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,
                                                                                                                                                                                                                                                                                                                                                   V66971;
14-JAN-1999 (first entry)
Mouse Ikaros encoding cDNA mIk-1.

GD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS; Alzheimer's disease; ss.
    cttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaaaacctt 325
                                  680 CCTTTACCCAGAAAGGCAACCTCCTGCGGCACATCAAGCTGCACTCGGGTGAGAAAGCCCT 739
                                                                                               TCAAATGCCATCTTTGCAACTATGCCTGCCGCGGAGGGACGCCCTCACCGGCCACCTGA 799
                                                                                                                                              920 cegecererececaercarraageaagaacraaccacaaceagaregecagaagacerer 979
                                                                                                                                                                                                                                                                                                                    ttaagtgtcacctctgcaactatgcatgccaaagaagagatgcgctcacgggggcatctta
                                                                                                                              ggacacattctgtggagaaaccctacaaatgtgagttttgtggaaggagttacaagcaga
                                                                                                                                                                                            gaagttcccttgaggagcacaaggagcgctgccgtacatttcttcagagcactgacc---
                                                                                                                                                                                                            ---caggggacactgcaagtgcggaggcaagacacatcaaag-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikaros poly:peptide(s) - useful for treating disorders of immune
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
223. .1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "mIk-1"
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US-946233.
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05-JUN-1995; US-465590
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WPI; 98-582621/49.
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CDNA clones (T16059 and T16061-64) encode different isoforms, mlx-2, mlx-3, mlx-1, mlx-4 and mlx-5; (R32014 and R92016-19). Fespectively), of the mouse Ikaros protein, a master regulator of hematopoietic differentiation. They were isolated from a mature colling to the Ikaros genomic locus. All include exons E1/2 and E7, but have different combinations of exons E3-E6 encoding a mutated Ikaros transgenic animals, pref. mice, having a mutated Ikaros transgene, esp. a mutation that alters the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccagtggaaagatgaactgcgatgtgtgtggattatcctgcatcagcttcaatgtcttaa 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 24; Gaps
                                                                                                                                         Ikaros; transgene; transgenic animal; transgenic mouse; mIk-1; immunocomprised; immune system disorder; nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determine the effects of treatments for immune or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.4%; Score 209.8; DB 1; Best Local Similarity 67.1%; Pred. No. 5.7e-58; Matches 339; Conservative 0; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 C;
818 AACGTAAGAGCTCTATGCCTCAGAAATT 845
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                               /*tag= b
/label= Exon-1/2
                                                                                                                                                                                                                                                                                                                                                                                                  /label= Exon-5
934. 1068
/*tag= f
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Exon-6
                                                                           T16062 standard; cDNA; 2049 BP
                                                                                                                                                                                                                                                                                                                    '*tag= c
label= Exon-3
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/label= Exon-7
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/label= Exon-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         069. .1776
                                                                                                                                                                                                                     223. .1779
/*tag=_a
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1995; U09345.
29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                  182. .642
                                                                                                                                                                                                                                                                                                                                               643. .810
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                                                                                                                                                                                                                                                    . 381
                                                                                                                            CDNA mIk-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georgopoulos K;
WPI; 96-129389/13.
                                                                                                                                                                        animal model; ss.
                                                                                                                          Murine Ikaros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; R92017
                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9604372-A1
                                                                                                        09-MAY-1996
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Claim: 1. Page 127-129: 158pp: English.

Claim: 1. Page 127-129: 158pp: English.

Claim: 1. Page 127-129: 158pp: English.

Codes for a 516-amino acid zinc finger protein (see W70971) that is involved in the early differentiation of lymphocytes. It was involved in the early differentiation of lymphocytes. It was involved in the early differentiation of lymphocytes. It was involved in the early differentiation of lymphocytes. It was controlled from a Jurkat T cell line library using mouse Ikaros exon throws as probe. The Ikaros gene maps between pli.2-pl3 on human chromosome 7. The human and murine Ikaros sequences (see V42805-11 and V42840) are highly conserved. Differential splicing of Ikaros proteins. These are used to treat T and B cells expressing Ikaros proteins. These are used to treat T and B cells expressing Ikaros proteins. These are used to treat T and B cells cancers), to control expression of heterologus genes placed under control of an Ikaros-responsive element, to treat nervous system cancers), to control of an ikaros-responsive element, to treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, amplication or differentiation, especially in haematopolette.

C cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences. The same effect can be achieved with Ikaros binding oligonucleotides. Examining the expression of the Ikaros gene, or its allelic structure, can be used to assess risk of acquiring the above diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 ccagiggaaagaigaacigcgaigigigigatiaiccigcaicagciicaaigiciiaa 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         578 GGACGCACTCCGTTGGTAAACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGC
                                                                                                             P-PSDB; W70971.
New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, related products, used to treat e.g. immune diseases or cancer to control cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1551;
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Pred. No. 3.7e-60;
0; Mismatches 136; Indels
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Best Local Similarity 67.9%;
Matches 345; Conservative
                   02-JAN-1997; 194256.
05-SEP-1996; US-711417.
(GEHO ) GEN HOSPITAL CORP.
                                                                          Georgopoulos K;
WPI; 98-378292/33.
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                                                                                            CTAACGGAAAACTAAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCA 232
                                                                                                                                                                                                         cttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaaaaactt 325
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                     Indels
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cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; ss.
 ed. No. 3.5e-60;
Mismatches 136;
   Pred. No.
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V42840;
11-JAN-1999 (first entry)
Human Ikaros isoform hik-1 cDNA.
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/*tag= c
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715. .849
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27. .163
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589. .714
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67.98;
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850. .1551
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                   Conservative
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   Similarity
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   Best Local
                   Matches
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Prepage with the control of lymphocytes - existing in several isoforms, and differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and related products, used to treat e.g. immune diseases or cancer and related products, used to treat e.g. immune diseases or cancer and related products, used to treat e.g. immune diseases or cancer and include of luman itaros cDNA (isoform hik-1) that codes for a 461-amino acid zinc finger protein (see W70964) that is involved in the early differentiation of lymphocytes. It was involved in the early differentiation of lymphocytes. It was isolated from a Jurkat T cell line library using mouse likaros exon chromosome? The involved processing income maps between pll.2-pl3 on human chromion provides rise to different insolation of and v42840) are highly conserved. Different isolation of expressing lkaros proteins. These are used to treat T and B cell diseases (e.g. immune deficiencies caused by drugs, radiation or concrol of an Ikaros responsive element, to treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, control of an Ikaros responsive element, to treat nervous system control of an Ikaros responsive element. The meamedopoletic cells. Some Ikaros isoforms are antaqonistic of others and may be used to inhibit interaction with DNA sequences. The same effect can be achieved with Ikaros-binding oligonucleotides. Examining the apprentice of the apprenticed on its and the control can be controled to the interaction with DNA sequences. The same effect can be achieved with Ikaros-binding oligonucleotides. Examining the apprentice of the can be controled to the controled of the co
                              Examining cture, can }
                                                     593 TGTGCAAGATAGGATCAGAGATCTCTCGTGGACAGACTAGCAAGTAATGTCGCCA
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                                                                                                                                                                                                                                                                                                                                                                                              Ikaros; hIK-1; transcription factor; human; lymphocyte; cell differentiation; T cell; cancer; immunodeficiency; Alzheimer's disease; therapy; diagnosis; ss.
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                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                11-JAN-1999 (first entry)
Human Ikaros isoform hIk-1 cDNA.
                                                                                                                                                                                                                                                                                               V42806 standard; cDNA; 1386 BP V42806;
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424. .549
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256. 423
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WPI; 98-378292/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                               Human Ikaros
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Disclosure; Column 55-58; Illpp; English.

The present invention describes a purified peptide having at least one
of the following properties: (a) it stimulates transcription of a DNA
sequence under the control of a delta A element, an NFKB element or an
ikaros binding oligonucleotide consensus sequence; (b) it binds to any of
a delta A element, an NFKB element or an ikaros binding oligonucleotide
consensus sequence; (c) it competitively inhibits the binding of a
adurally occurring ikaros isoform to any of a delta A element, an NFKB
element or an ikaros binding oligonucleotide consensus sequence; (d) it
competitively inhibits ikaros binding to ikaros responsive elements; or
(e) it inhibits protein protein interactions of transcriptional complexes
formed with naturally occurring ikaros isoforms. The proteins, provided
that they stimulate gene transcription under the control of delta A
elements, NFKB elements and/or ikaros binding oligonucleotides, bind
delta A elements, NFKB elements and/or ikaros-binding oligonucleotides,
competitively inhibit ikaros binding to ikaros-responsive elements and/or
competitively inhibit ikaros binding to ikaros-responsive elements and/or
competitively inhibit ikaros binding to ikaros-responsive elements and/or
contenting interactions of transcriptional complexes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence encodes a specifically claimed human Ikaros protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaaaacctt 325
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                                                                                                                                                                                                                                                                                                                                                  Ikaros poly:peptide(s) - useful for treating disorders of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 216.4; DB 1;
Pred. No. 3.5e-60;
0; Mismatches 136;
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                                                     /product- "Ikaros"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.5%;
Best Local Similarity 67.9%;
Matches 345; Conservative (
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1. .1386
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US-238212.
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05-JUN-1995; US-465590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1386 BP;
                                                                                                                                                                                                                                                                           Georgopoulos K;
WPI; 98-582621/49.
                                                                                                                                                                                                                                                                                                                         P-PSDB; W72672
                                                                                                                        05-JUN-1995;
02-MAY-1994;
                                                                                                                                                                         14-SEP-1992;
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Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severally immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders. Disclosure; Fig 2: 102pp; English.

Chalmost full-length cDNA sequence (T16060) codes for part (R92015) of the human Ikaros protein, a master regulator of haematopoietic differentiation. It was isolated from a T-cell in Jurkat cDNA library using a mouse Ikaros cDNA clone as probe. The human Ikaros gene maps to pll 2-pl3 on chromosome 7.

Chief profit isoforms (see R92014 and R92016-19) of mouse Ikaros have also been isolated. Transgenic animals, pref. mice, having a mutated ikaros transgene, esp. a mutation that alters the DNA binding domain of the Ikaros protein, are used as models to determine the effects of treatments for immune or nervous system
                                                                                                                                                                                                                                                                                                                           CTAACGGAAAACTAAAGTGTGATATCTGTGGGATCATTTGCATCGGCCCAATGTGCTCA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAAATGCCACCTCTGCAACTACGCCTGCCGCGGGGGACGCCCTCACTGGCCACCTGA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS; Alzheimer's disease; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                            ccagtggaaagatgaactgcgatgtgtgtggattatcctgcatcagcttcaatgtcttaa
                                                                                                                                                                                                                                                                                                                                                                           gaagtteeettgaggageacaaggagegetgeegtacattetteagageactgace--e
                                                                                                                                                                                                                                                                                                                                                            206 tggttcataagcgaagccatactggtgaacgcccattccagtgtaatcagtgtggggcat
                                                                                                                                                                                                                                                                                                                                                                                                            266 cttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaaaaacctt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 GAACGICITIAGAGGAACAIAAAGAGCGCIGCCACAACIACIIGGAAAGCAIGGGCCIIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 CGGCCACACTGTACCCAGTCATTAAAGAAGAACTAAGCACAGAGAATGGCAGAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttaagtgtcacctctgcaactatgcatgccaaagaagagatgcgctcacgggggcatctta
                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                              Length 1386;
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                                                                                                                                                                                                                                                           Score 216.4; DB 1; Length 1
Pred. No. 3.5e-60;
0; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggggacactgcaagtgcggaggcaagacacatcaaagca----
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                                                                                                                                                                                                                         403 C;
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Human Ikaros encoding cDNA
                                                                                                                                                                                                                                                                                      Matches 345; Conservative
                                                                                                                                                                                                                          BP;
                                                                                                                                                                                                                                                                        Similarity
Georgopoulos K;
WPI; 96-129389/13.
                                                                                                                                                                                                                         1386
                        P-PSDB; R92015.
                                                                                                                                                                                                            disorders.
Sequence
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Best Local S
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                                                                                  395 CTAACGGAAAACTAAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCA 454
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                                     Gaps
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disorder;
                                                                                                                                                                                   CATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCT
                                                                                                                                                                                                                                                                                                                                                                                   CGGGCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGACC
                                   27;
            Length 1611;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ikaros; transgene; transgenic animal; transgenic mouse; immunocomprised; immune system disorder; nervous system animal model; ss.
          Score 216.4; DB 1;
Pred. No. 3.7e-60;
0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/*tag= a

/*tag= bxon-3

256 .423

/*tag= b

/label= Exon-4

424 .549

/*tag= c

/*tag= c
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/*tag= d
/label= Exon-6
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/label= Exon-7
          Query Match
34.5%;
Best Local Similarity 67.9%;
Matches 345; Conservative
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T16060;
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28-JUL-1995; U09345.
29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Ikaros cDNA hIk-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A cDNA clone (160490) corresponds to the mouse Aiolos gene, a cDNA clone (160490) corresponds to the mouse Aiolos gene, a holos cDNA was isolated from a mouse spleen cDNA library using a probe that spanned nuclectides 796-1156 of the sequence.

Aiolos (W15574) can form dimers with Aiolos or Ikaros polypeptides, is expressed in committed lymphoid progenitors and in T and B cells, and is a transcriptional activator of a lymphoid gene. Primers (see also T60494-95) based on mouse Aiolos gene exons were used to may library a human partial Aiolos cDNA (see also T60491). Aiolos CDNA can be used to produce recombinant Aiolos in transformed host cells. The Aiolos polypeptide, coding sequence or cells expressing Aiolos CDNA can be used to treat a disorder in an animal, esp. by gene therapy. Such disorders include T-cell leuksemias and lymphomas. Transgenic animals are provided with an Aiolos transgenic canimals are provided with an Aiolos transgenic Sequence 1984 BP; 512 A; 570 C; 535 G; 367 T;
                          540
                                                                                                                                                     Aiolos polypeptide and corresponding DNA - used to reconstitute a mammalian immune system, for the treatment of T cell leukaemia(s)
                                                                                                                                      acatttcttcagagcactgacccaggggacactgcaagtgcggaggcaagacacatcaaa
                                                                                                                                                                                              78.6%; Score 493.6; DB 1; Length 1984; 87.7%; Pred. No. 1.2e-149; ive 0; Mismatches 74; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                             Aiolos; transcription activator; immune system; T lymphocyte; B lymphocyte; leukaemia; lymphoma; asthma; gene therapy; transgenic animal; ss.

Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and lymphoma(s)
Disclosure; Page 73-76; 115pp; English.
                                                                                                                                                                                                                                                   cgaaaaagctcaatgcctcagaaattca 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 374. .1897
                                                                                                                                                                                                                                                                T60490 standard; cDNA; 1984 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georgopoulos K, Morgan BA; WPI; 97-245047/22.
                                                                                                                                                                                                                                                                                                                                                                         07-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 87.7 Matches 551; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCI-1995; US-005529.
14-MAY-1996; US-017646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-1996; U16774
                                                                                                                                                                                                                                                                                                                                                                                          Mouse Aiolos cDNA.
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ccttacagctattcaagagaatataatgaatatgaaaacattaagttggagagacatgtt 120
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ing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treell pathway regulatory gene, Ikaros - encodes family of unique zinc finger proteins, useful for treating immune system disorders claim 13: page 44-46; 112pp; English.

The Ikaros gene encodes a zinc finger protein which can be used in therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is a risk for an immune disorder. It is of particular use in treating a Sequence 1611 BP; 375 A; 484 C; 480 G; 272 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder; therapy; treatment;
                                                                                                         241 ttccaqtgtaatcaqtgtggggcatctttactcagaaaggtaacctcctccgccacatt
                                                                                                                                                                                                                                                                                                                                 421 ttttgtggaaggagttacaagcagaagttcccttgaggagcacaaggagcgctgccgt
                                                      806 TICCAGIGIAAICAGIGGGGGGAICITITACICAGAAAGGIAACCICCTCCGICAIAII
                                                                                                                                                                                                                                                                                                                                                                                      481 acatttcttcagagcactgacccaggggacactgcaagtgcggaggcaagacacatcaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a /product= Peptide with Ikaros activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1166 CGAAAAGCTCGATGCCTCAGAAATTCA 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-001-1994 (first entry)
Human Ikaros peptide coding sequence.
Ikaros; zinc finger; protein; immune d
corpus striatum; regulatory gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 cgaaaaagctcaatgcctcagaaattca 628
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Q44980;
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14-SEP-1992; US-946233.
(GEHO ) GEN HOSPITAL CORP.
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P-PSDB; R46964.
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1 gaaagagatgagaatgttttaaagtcagaacccatgggaaatgcagaagacctgaaatc 60

Genetic locus bcl-TRP-1 protein codi

Q80513 T42903

0.6

56.6 56.4

44

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

November 6, 1999, 02:38:40 ; Search time 70.34 Seconds (without alignments) 2233.731 Million cell updates/sec Run on:

US-09-019-348-7 628 1 gaaagagatgagaatgtttt.....ctcaatgcctcagaaattca 628 Title: Perfect score: Sequence:

Scoring table: IDENTITY_NUC

311585 seqs, 125096042 residues N_Geneseq_36:* natahase : Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Alolos	Alolos cDNA	Ikaros	Trains	Tkaros e	Tkaros	e Ikaros	Ikaros e	e Ikaros i	e Ikaros	Ikaros	e Ikaros	Ikaros i	e Ikaros	Ikaros e	Ikaros i	e Ikaros	Ikaros e	Ikaros	CDNA. T	s isofor	Ikaros cD	protein	s protein		Human gene signatu	ic can	secre	uman gene	lone A	brain .	SRE-ZBP	SRE-ZBP a	OTK18 gen	an OTK18 ge	encoding	encoding an a	inc finger pro	one CO1069	yc-binding zin	s protein en	cell z
SUMMAKIES	ID		0049	2.40	D (000071	200	284	T16062	697	280	044979	605	969	280	90	3	စ္က	90	37	စ္က	9	93	37	2	12	996	37	973	064	534	658	98	348	φ	.v01890	33	53	9	97	978	V64579	712	136
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d	Query Match	; ;			·	· • •	* 4		33.4	Э.	m	7.	27.1	۲.	7	m.	m.	m.	7	۲.	۲.	۲.	7	۲,	٠,	٠ و	ij	٠.	٠.		0		٠.			٠		٠	٠		٠			•
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	Result No.		- 1 (71 (n <	* u	י ע	, ~	8	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	58	67	30	3.1	32	ED :	34	32	36	37	38	39	40	41	42	43

	ALIGNMENTS
<u> </u>	RESULT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
HA	ID T60491 standard; cDNA; 628 BP.
<u> </u>	07-JUL-1997 (first e
- X	<pre>Human Alolos partial cDNA. Alolos; transcription activator; immune system;</pre>
	KW B lymphocyte; leukaemia; lymphoma; asthma; gene therapy; KW transgenic animal; ss.
ŏ	Homo sapiens
- A	
<u> </u>	
·	PA (GEHO) GEN HOSPITAL CORP.
. <u>6</u>	
ā ā	P-PSDB; W15575. Minios nolymentide and corresponding DNA - used to reconstitute
à	mammalian immune system, for the treatment of T cell leukaemia
Δ, ř	and lymphoma(s)
- -	Partial human Aiolos CDNA (1
5	amplification using primers (see also T60494-95) based
ŏ č 	Aiolos gene exons. The Aiolos gene is a homologue of
∵ —	can form dimers with Aiolos or Ikaros polypeptides, i
ŏ	committed lymphoid progenitors and in T and B cells, and is a
ŏč —	transcriptional activator of a lymphoid gene.
—	cells. The Aiolos polypeptide, coding sequence or cell:
შ ≀	Aiolos may be used to treat a disorder in an animal, esp. by gene
ซ ซ	therapy. Such disorders in Non-wildtype gene structure
ŏ	for such a disorder. Transgenic animals with an Aiolos tran
ñ	equence
	atch 100.0%; Sc
	28; Conservative 0; Mismatches 0
8	Qy 1 gaaagagatgagaatgttttaaagtcagaacccatgggaaatgcagaagagcctgaaatc 60
ñ	DD 1 GAAGAGATGAGAATGTTTTAAAGTCAGAACCCATGGGAAATGCAGAAAGGCCTGAAATC 60
	5
× 7	
<u></u>	19
ð'	Qy 121 gtctcattcgatagtagcaggccaaccagtggaaagatgaactgcgatgtgtgtg
<u>ā</u>	Db 121 GTCTCATTCGATAGTAGCAGCCCAACCAGTGGAAAGATGAACTGCGATGTGTGTG
<i>6</i> '	Oy 181 tcctgcatcagcttcaatgtcttaatggttcataagcgaagccatactggtgaacgccca 240
	Db 181 TCCTGCATCAGCTTCAATGTCTTAATGGTTCATAAGGGAAGCCATACTGGTGAACGCCCA 240
ි 	Oy 241 ttccagtgtaatcagtgtggggcatctttactcagaaaggtaacctcctccgccacatt 300
<u>ត</u>	Db 241 TICCAGIGTAATCAGIGIGGGCCAICTITIACICAGAAAGGIAACCICCICCGCCACAII 300
ö'	Oy 301 aaactgcacacaaggggaaaaaccttttaagtgtcacctctgcaactatgcatgc
_	

Search completed: November 6, 1999, 06:39:51 Job time: 4705 sec

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EWGNNYTHCGPCAS.YUTCPVCAS.HTSCHREEELLLQCQYCDRWYHAVCESLYTEDPVEQAS
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FAQLAGETTLDGQPIERTIDEDNIMDPRPAEGGEGQAKKRRGKKERMRGKKEDMRFPATLQCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIPOGAS PRESECT KIGSPSHPPESSLIPROSGONGSLGPORHPTNOGENOPRUPS SPOSISONS COST PRESECTION OF SPOSISONS COST PROSECTION OF SPOSISONS COST
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FRKVLGVSDGSSLGGMKPILESSKGESHTALPQSALLPGSLPSAEMVDAFPGLSQSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDMRDRGGLFSPDGGEESPWATPSTPVTPSSPTPTETEGGGLSYNORSLORWEKDEE
TGELSTISPYVLXANTNRPPTLKRDYPDWASRCKQUMKYNKKASADKVPYLQKAKDDRA
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LPDSGSSSVFFSDGPVRTPGSAEIRTDPLAKFPPQSPHCHSHPPFFSHAGASPLQAS
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SHMGPQAASSSPNVGTVQSQLPPQSVVTRPQPTTVENSEELPEPDLEGLGDASADGGV
EDEDDLALDLDPDKGDDDLGNLDNLETNDPHLDDLLNSDEFDLLAYTDPELDQGDPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSGYVPSGPQGPPQGRPASLGPFDMQPGTPGTPRRAQQVDPYFRSQLQKQGHLPQTQ
QGSQESLAPPGSPHSRVAGIGESPLFSPSHSTHYGDAFRNQQGMGRPEYGSSPSHSGQ
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ASSSTHIESVQVCALCNCVEWSLHGQRELRYFGPFSEWRTLQPSSTPLPQPGNDDLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDPLREERCLVIKQELQEQKIKPDLLLDETSNLSHGDESSGFLGSPGEPDAHLSMEF
GLESGAHSHADNLLTETDDSLPFEPLRSDREKVKRRGSPGRSRMKQSRSSGFPGRRRP
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PKEEETERAISPIIPLIPRTAIPAFPEYKPLEGSDSKVASTSNHWEKAKSNEVSVTLT
                                                                                                                                                                                                                                                                                                    IGFSVLPCLAALLDDSGGGWVHHWCÄVWSEGVKQHENDKLKDVDKAVISGIPRLCEHC
KRLGATIQCHAEGGSRFYHFPCSAASGSFQSWKQLLLLCPEHIDKAKELGEEACCAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                DSAGELSDLLFCTGCGQHYHAACLEIGATPIQRAGWQCPECKVCQTCRKPGEDSKMLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDACDKGYHTFCLOPAMDSLPTDPWKCKRCRVCTDCGARGLELPGSTQWFENYAVCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CQHHRNCTCSVCNK PDGSVATLQSCSVCHRLVHSGCTLFKELSEDKCÍCLHCKEQLPV
TQPHTAEIQTREAPEDTAGRVDLIEMTIQTDAAMTTEEHMDVPEVTPRHKSLAETDQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EASANTETPMDLGPDQKETTSSVEQQAELLKSNHDVWPVTNQLGTSLPHSEEEEDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGGGGGGGGGRGRSTLKAMASCIDALSMASDTGVTKEEEEEDDTMQNTVVLFSNTDKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QALMAAGGRVQGSPSHAYSPRGPFGMSPVHPASPNSSHASSPSMGDGRAGRGSPYNQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLIKQLKQGLSLLPLMEPSITASLDLFAPFGSSPANGKAQLKGSFGNAVLDNIPDYYS
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VVFLYNMMFAGLTGASLIKTFTHAVQNELITRAFGEFYCHFHHLRSFS"
John (51200. 51357,51796. 51935,52407. 52699,52820. 52996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(35069. .35826,35902. .36163,37759. .38067))
/gene="fhh"
                                                                                                                                                                                NIDVDLWVHLNCALMSTEVYETGGGALMNVEVALRRGLRTLCAFCGKTGATNSCNRLR
CPUNYHRFGATRANLRRYENSKTMLCYOHKLKGPSEDELSLFAVLRRYETBEDEWGIA
STLORGDR.HILFRVGGLIFRANCOLLSOMANFHSFTATIFPVGYEATRIYMSTRLPNR
RCRYRCRISEDDGRPLFEVRVLEHGMEDLQFRDCTPEGIWNQVVQKVAQLREESSMLK
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SEPRVSTOKRRPHTNSTSVSKRAYGSTFTGELNTPYSKQFVHSKSSOYRRLXFEWKNN
VYLARSRIGGLYAARDLEKHTMVIEYIGTVURNEVANRREKIYESONRGIYMFRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVEVDGVLASSYALVEDHQLAHWAFGPVRLLSSVSQLLWAEPEERSDGSKTPLQPHAL
VRGDRKVCARNSTSVRSEAGPRGRTSEVHWYAQLLHRLGWIVLNPDLFHP"
complement (join (44074. 44279,44841. 44997,44991. 45081,
45174. 45247,4519. 45402,45477. 45587,75659. 45720,
45809. 45881 45595. 46029,46116. 46184,46269. 46392,
46486. 46589,46846. 46985,47262. 47345,48176. 48315))
/note="similar to Caenorhabditis elegans R05b3.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Translation-*MOTCKLKMHETPLCLLQICVLLFTCLYIVCYLILTHFKKTAEFV
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NMEAMQKEYQAVYHHLSSYVLTEMRRKASPWQRNLGYPLAMLTLLALLYWCVLMVCIN
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DSGAAADAAQPADLGEPGPPESDAAAAPCADPEPAAPADVLPNVKKWKGIRWKRLPI
VISIRKGSSKKETSREVSELMESLRITLRPERLPRDKRKCCFCHEEGDGATDGPARLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGLLAQLAVEAGFDWVHYESKYHIHCSVKADHSVAVEKGGCFPGWSRVTVAGGFQKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC34386.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEOVIDATLIGGPARYVNHSCAPNCVAEVVTFDKEDKIIIISSRRIPKGEELTYDYOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKQCWWARLAQVSLLAAWSCVWLVQGCGPGPGYGIRTRPRKLKA
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KRCKDCLNRLALAVMNQWPGVHLRVTEAWDEDGHHPPGSLHYEGRAVDITTDDRETEK
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LSSAAAKKLNHVMMAMAQLLNIQMPGSYELSFPPQNPDMADFDGPGKGPGQSALGLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56155 AACCTGCTGCCGCCACATTAAGCTACACTCAGGAGAAGCCTTTCAAATGCCCCATCTGC 56214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56095 CTTACAGGTGAAAGGCCGTTCCAGTGTAACCAGTGTGGGGCCTCCTTCACGCAGAAGGGA 56154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 aacctcctccgccacattaaactgcacacaggggaaaaaccttttaagtgtcacctctgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(35069. .38067)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAc34385.1"
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/db_xref-"GI:3170537"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="fhh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
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                                                                                                                                                                                               KEYWORDS
SOURCE
ORGANISM
                                                                                  DEFINITION
                                   RESULT 15
AF056116
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REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="memeraquegroppendyseendeamplpedlsassnld"
HNNRGDKEGLERPECCTGCGASFTOKGNLLRHIKHSGEFFFKGHLCNYACRRDAL
SGHLRTHSVGRPHKGAYCGRSYKORSSLEEHKERCHNYLOCMGLONIYTGERRFSNL
SFEGGPELMOPHYLDQAINSAINYLGABSLRRLIGTSPTSSDMGYWGSMYELHKFPN
EGHGLSAKDSAAENLLLAKSKSASSEKDGFPSHSQDSTDTESNNEEKAGVGASGLI
YLTHHITSGYRNGVLPLYKEGOROKYPANRASIELASEGFKVLSGEGEGVRAYKCEHC
STILFLDHYWYIHRGEHRPPFECNLCGHRSQDRYEFSSHWTRGEHRY"

500 c 464 g 521 t 1 others
                                             Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 2079)
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                                                                                                                                             Isolation and characterization of Ikaros homologues in the rainbow
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Ik-8 isoform; similar to mouse and human
Ikaros/LyF-1; alternatively spliced form missing exons 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Submitted (06-MAR-1997) Comparative Immunol., Basel Inst. for
Immunology, Grenzacherstrasse 487, Basel CH-4005, Switzerland
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         /organism="Oncorhynchus mykiss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="lkaros homolog"
/protein_id="AAB53433.1"
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/db_xref="GI:2062738"
                                                                                                                                                                                                                                                                                                                                                     /cell_type="thymocyte"
81. .1232
                                                                                                                                                                                                                                                                                                                        /strain="shasta"
/db_xref="taxon:8022"
                                                                                                                                                                                                                                                                                                                                                                                          /gene="Ikaros"
81. .1232
                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Ikaros"
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Hansen, J.D.
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   GI:2062737
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                               rainbow
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Best Local Simil
Matches 215; (
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/clone="29914; 3A8; 138E3; 186G5; 178023"
/note="sequenced from overlapping cosmids of the HGMP Fugu
cosmid library"
join(449. 545,702. 943,1038. .1281,1393. .1623,1735. .1902,
2006. .2162,2229. .2353,2432. .2562,2649. .2774)
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On Jun 2, 1998 this sequence version replaced gi:1814290.
Prediction of protein sequences are solely based on homology search analysis and XGRAIL analysis of the genomic DNA sequence.
Location/Qualifiers
1. 146840
/organism="Fugu rubripes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="serine/threonine kinase receptor typel"
/protein_id="AAO34382.1"
/db_xref="PID:3170555"
/db_xref="101:3170535"
/translation="MIQWRHEGRSFLLLLGFITYTSHWAASSQSVCLALRCNCTNCEKT
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CNSIDLKVPGKEGGWASSSWGPVELVAVIAGPVFLLCVLLMVGVFLFQYHQRAYSHRQ
                   Fugu rubripes serine/threonine kinase receptor typel, All-11slated protein (ALR), fugu hedgehog (fhh), Ikaros-like, wntl, wntl0b, ARR3, erb83, PAS1, and L41 ribosomal protein genes, complete cds; ARP056116 U82608
                                                                                                                                                                                                                                                                                                                                           Fugu rubripes.
Fugu rubripes.
Fugu rubripes
Fugu rubripes
Eukaryota: Metascoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
Gellner, K. and Brenner, S.
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FGEVWRGKWRGGDVAVKIFSSREERSWFREAEIYQTIMLRHENILGFIAADNKDNGTW
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RDLKSKNILVKKNGMCAIADLGLAVRHESITDTIDIAPNQRVGTKRYMAPEVLDETIN
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QKLRPNVPNWWQSYEALRVMGKIMRECWYANGAARLTALRIKKTLSQLSVEEDIKM"
complement(7874. .29042)
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   15-APR-1999
   VRT
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   DNA
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148640 bp
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ALTEL AT 1 CONTROL OF THE CONTROL OF
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/note="Ik-2 isoform; similar to mouse and human
Ikaros/LyF-1; alternatively spliced form missing exon
/codon_start=1
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                                                 mykiss"
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Pred. No. 1.8e-37
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                             /product="Ikaros homolog"
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/db_xref="PID:92062740"
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                                                                                                                       /cell_type="thymocyte"
50. .1336
                                                                                                   /db_xref-"taxon:8022"
Location/Qualifiers
                                                                                                                                                                           /gene="Ikaros"
50. .1336
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Best Local Similarity 64.9%;
Matches 276; Conservative
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                                                                                                                     /product-"Ikaros homolog"
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RDALSGHLRTHSVGKPHKCGYCGRSYKQRSSLEEHKERCHNYLOSIGLOGHLYAVKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rainbow trout.
Oncorhynchus mykiss
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Actinopterygii;
Bopterygii; Teleostei; Euteleostei; Protacanthopterygii;
Salmoniformes: Salmonidae; Oncorhynchus.
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  <1. .>415
//gene="IKaros"
//oce="similar to mouse and human Ikaros/LyF-1; composed
of exons 4, 5 and 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-1997
Ik-2 isoform,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcatgccaaagaagaagatgcgctcacgggggcatcttaggacacattctgtggagaaaccc 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tacaaatgtgagttttgtggaaggagttacaagcagagaagttcccttgaggagcacaag 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctccgccacattaaactgcacacaggggaaaaaccttttaagtgtcacctctgcaactat 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GAGAGATGTCACAACTACCTACAAGTATAGGCTTGCAGGGCCATCTTTATGCTGTAAAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---gcagagatgggaagtgaaagagctctc 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GAAGAGAGCAAAATTGATATGGCAGAAGACCTGTCCAAGATTGGGTCAGAGAGATCACTT 360
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Hansen, J. D.
Direct Submission
Submitted (06-WAR-1997) Comparative Immunol., Basel Inst. for Immunology, Grenzacherstrasse 487, Basel CH-4005, Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Gaps
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Oncorhynchus mykiss Ikaros homolog (Ikaros) mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 166.2; DB 4;
Pred. No. 1.4e-37;
0; Mismatches 123;
                                                                                                                                                                                                                                                                                                         100 g
                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.5%;
Best Local Similarity 65.3%;
Matches 271; Conservative
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U92200.1 GI:2062739
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Hansen, J.D.
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DAVDNLLLLSKAKSVSSEREASPSNSCQDSTDTESNNEEQRSGLIYJTNHINPHARNG
LALKEEQRAYEVLRAASENSQDAFRVVSTSGEQLKVYKCEHCRVLFLDHVMYTIHMGC
                                                        1165 AGTGTGGTGCCTCCTTCACACAGAAGGGCAATCTGCTTCGCCACATCAAGCTGCACTCGG 1224
                                                                                                                                                                                                                                                                                  1285 CTGGCCACCTCCGCACACACTCCTCCTCCCCCACCGTGGGCAAACCCTACAAGTGCA 1344
             313
                                                                                                                                                                                                                                                      418
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 1550) Georgopoulos, K., Moore, D.D. and Derfler, B. Ikaros, an early lymphoid-specific transcription factor and a putative mediator for T cell commitment Science 258 (5083), 808-812 (1992)
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DNA-binding transcription factor; Ikaros, Ikaros DNA binding protein; transcription; zinc finger protein; zinc-finger transcription factor.

Mus musculus (library: Lambda ZAP EL4) adult cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete cds
                                                                                                                         agtgtggggcatcttttactcagaaaggtaacctcctccgccacattaaactgcacacag
                                                                                                                                                                                                                                                  374 cggggcatcttaggacacatt------ctgtggagaaaccctacaaatgtg
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Mouse Ikaros DNA binding protein (Ikaros) mRNA,
L03547
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39. .1334
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/gene="Ikaros"
39. .1334
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                                                                                                                                                                                                                                                                                                                                                                                                     1405 ACAACTACCTACAGAG 1420
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MUSIKAROS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                         289 ctccgccacattaaactgcacacaggggaaaaacttttaagtgtcacctctgcaactat 348
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Ikaros homolog (Ikaros) mRNA, partial cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 CACAAATGTGGATATTGTGGCCGGAGCTATAAACAGCGGAAGCTCTTTAGAGGAGCATAAA 437
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2 (bases 1 to 415)
Hansen,J.D.
Direct Submission
Submitted (06-WAR-1997) Comparative Immunol., Basel Inst. for Immunology, Grenzacherstrasse 487, Basel CH-4005, Switzerland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 tacaaatgtgagttttgtggaaggagttacaagcagagaagttcccttgaggagcacaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 GAAGAAACTAACCACAACGAGATGGCAGAAGACCTGTGCAAGATAGGAGCAGAGAGGTCC
                                                                                                                     Length 1550;
                                                                                                                                                               24;
                                                                                                                 Query Match 27.3%; Score 171.6; DB 12; Length Best Local Similarity 67.3%; Pred. No. 3.8e-39; Matches 284; Conservative 0; Mismatches 114; Indels
HGCHGFRDPFECNMCGYHSQDRYEFSSHITRGEHRYHLS"
431 c 423 g 311 t
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Xenopus laevis/gilli
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09-APR-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hommia, Y., Kiyosawa, H., Mori, T., Oguri, A., Nikaido, T., Kanazawa, K., To'o, M., Takeda, J., Tanno, Y., Yokoya, S., Kawabata, I., Ikeda, H. and Wanaka, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (II-SEP-1998) to the DDBJ/EMBL/GenBank databases. Akio Wanaka, Fukushima Medical College, Institute of Blomedical Sciences, Department of Cell Science; Hikarigaoka I, Fukushima, Fukushima 960-1295, Japan (E-mail:wanaka@cc.fmu.ac.jp, Tel:81-24-548-2111(ex.2800), Fax:81-24-549-8898)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predominantly expressed in the
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                  aagtgaaagagctctcgtactggacagattagcaagcaatgtggcaaaacgaaaagctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eos: a novel member of the Ikaros gene family expressed predominantly in the developing nervous system FEBS Lett. 447 (1), 76-80 (1999)
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Pred. No. 2.1e-40;
0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                   AB017615 2688 bp mRNA ROD MUS musculus mRNA for Eos protein, complete cds. AB017615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eos protein.
Mus musculus (strain:ICR) Newborn cDNA to mRNA.
Mus musculus
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794 c 673 g 620
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/strain="ICR"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:4062982
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753.
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/gene="Eos"
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Matches 261; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wanaka, A.
Direct Submission
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958 TATGCCACAGAGGTT 972
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                                                                                                                                        612 aatgeeteagaaatt 626
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/db_xref="PlD:93661583"
/db_xref="PlD:9361583"
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SLRPLVQTSPGSADMYVSPLYNLHKSGTAEGNGVSAKDSAABHLLLLSKSKGANSVDKD
GESPPSGQDSTDTESNNEERSGVSGTAATGGLIYLTNHMAPGMRNGGLPGVKEEQQR
HFEALRAAGMDLSIASSEGFKVLSGDGEELRAYRCIHCRVLFLDHYMYTIHMGCHGFR
DPFECNLCGYRSQDRYEFSSHITRGEHRI
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                                                                                                                                                                                                                   Ameniya,C. and Kawasaki,H.
Direct Submission
Submitted (15-SEP-1998) Center for Human Genetics, Boston
University School of Medicine, 715 Albany Street, Boston, MA 02118, USA
Neopterygii: Teleostei: Euteleostei: Ostariophysi; Cypriniformes;
Cyprinoidea: Cyprinidae: Rasborinae; Danio.
1 (bases 1 to 2309)
Amemiya,C. and Kawasaki,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 -------ggtgaacgcccattccagtgtaatcagtgtggggcatcttt 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 CACTCAGAAGGGTAACCTGCTCCGACACATCAAACTTCACTGGGGAGAAAACCTTTCAA 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         558 ATGICACCIGIGGAACTAIGCIIGCGGCGCAGAGACGCICICACIGGACAICIGCGCAC 717
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Pred. No. 1.3e-41;
0; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Danio rerio"
/db_xref="taxon:7955"
/tissue_type="spleen"
86. 1699
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"1karos"
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Best Local Similarity 62.3%;
Matches 346; Conservative (
                                                                                                                                                                                                  (bases 1 to 2309)
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                                                                                 AUTHORS
TITLE
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JOURNAL
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Gaps

15;

Length 2688;

Box

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/product="multi-zinc finger protein helios"
/product="multi-zinc finger protein helios"
/protein_id="AaC00513.1"
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LHSGERFFFFCPPCSYRCREDAITGHLRTHSVGRPHKCNYCGRSYRQRSSLEEHKERC
HNYLQNVSMEAAGQVMSHHVPPMEDCKEQEPIMDNNISLVPFFFRPAVIEKLTANMGKR
                                                                                                                                                                                                                                                                                                              KSSTPOKFVGEKLÄRPSYPDIHFDMNLTYEKBAELMOSHMMDQAINNAITYLGABALH
HDQIARPTIAEVAPVISSAYGOYHPHRIERPISTBFTSBFBNMDGPPSLIRPKSR
POEBERASPSNSCLDSTDSESSHDDROSYGGRPALNPKRKQSPAYMKEDVWALDATKAP
KGSLKDIYKVPNGEGEQIRAFKCEHCRVLFLDHVMYTIHMGCHGYRDPLECNIGGYRS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
     Direct Submission
Submitted (22-JAN-1998) HHMI/M&I, UCLA, 675 Circle Drive South,
951662, Los Angeles, CA 90095-1662, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1847;
                                                                                                                                                                                                                                                                                                                                                                                           517...834
/note="encodes N-terminal zinc finger domain"
1594...1746
/note="encodes C-terminal zinc finger
domain/hunchback-like zinc fingers"
a 466 c 445 g 402 t
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                                                                                                                                  /note="Ikaros family member"
                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
178. 1758
                                                  Location/Qualifiers
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                                                                                                                                                    /codon_start=1
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Best Local Similarity 70.6'
Matches 254; Conservative
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     TITLE
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AF092175
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OKFLDKCLSDMPYDSANYEKEDMMTSHVMDQAINNAINYLGAESLRPLVQTPPGSSEV
VPISSMYQLHRPPSDCPPRSHNSAODONVDULLLSKRKSVSTREASPENSCODSTD
TESNAEEQRSGLITITINHINHARNGLALKEEDRAYEVLRAASENSQDAFRVYSTSGE
OLKVYKCEHCRVLFLDHVMYTIHMGCHGFRDPFECNMCGYHSODRYEFSSHITRGEHR
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Mus musculus multi-zinc finger protein helios mRNA, complete cds.
92820276
AF044257.1 GI:2829276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttaagtgtcacctctgcaactatgcatgccaaagaagagatgcgctcacggggcatctta 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 TCAAATGCCATCTTTGCAACTATGCCTGCCGCGGAGGACGCCCTCACCGGCCACCTGA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542
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                                                                                                                                                                                                                                                                                                                                                                                                             tggttcataagcgaagccatactggtgaacgcccattccagtgtaatcagtgtgggggat 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cttttactcagaaaggtaacctcctccgccacattaaactgcacacaggggaaaaacctt 325
                                                                                                                                                                                                                                                                                                                                           146 ccagtggaaagatgaactgcgatgtgtgtggattatcctgcatcagcttcaatgtcttaa
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                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                           Score 197; DB 12; Length 684;
Pred. No. 2e-46;
0; Mismatches 140; Indels 2
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Matches 338; Conservative
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/brotein_id="Aaab3432.1"
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/db_xref="GI:2062736"
/db_xref="GI:2062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 2301)
Hansen, J.D.
Isolation and characterization of Ikaros homologues in the rainbow
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Ik-7 isoform,
ggacacattctgtggagaaaccctacaaatgtgagttttgtggaaggagttacaagcaga 445
                                                                                              446 gaagttcccttgaggagcacaaggagcgctgccgtacatttcttcagagca--ctgaccc 503
                        638 GCAGCICITIGGAAGAACAIAAAGAACGCIGICAIAACIACCIGCAAACCAIGAGIAICI 697
                                                                                                                                                                                                                                                     598 CAAGCAATCITTATTCAGTCATAAAGAGGAAACTAACCAGAGTGAAATGGCTGAAGACC 757
                                                                                                                                                                                                                                                                                                                                        758 IGTGCAAGATAGGGTCAGAAAGATCCCTCGTGCTGGATAGACTAGCAAGTAACGTCGCCA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (06-MAR-1997) Comparative Immunol., Basel Inst. for
Immunology, Grenzacherstrasse 487, Basel CH-4005, Switzerland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        /gene="Ikaros"
/note="Ik-7 isoform; similar to mouse and human
Ikaros/LyF-1; alternatively spliced form missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMU92198 2301 bp mRNA VRT ONCOTAYNCHUS mykiss Ikaros homolog (Ikaros) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="shasta"
/db_xref="taxon:8022"
/cell_type="thymocyte"
36. .1469
                                                                                                                                                                                                                                                                                                                                                                                                                                      1111 | 1 | 1111 | 1111| 1111| 815
818 AACGTAAGAGCTCTATGCCTCAGAAATT 845
                                                                                                                                                                                                                                                                                                                                                                                                                 aacgaaaaagctcaatgcctcagaaatt 626
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36. .1469
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U92198.1 GI:2062735
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386
                                                                                                                                                                                                                                                                                                        545
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/note="This sequence comes from Fig. 7A."
/codon_start=1
/exception="Protein longer than coding region shown"
/product="lymphoid transcription factor LyF-1 isoform VI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S74708 684 bp mRNA 12-MAY-1995 Ikaros/LyF-1-lymphoid transcription factor LyF-1 isoform VI [alternatively spliced] [mice, RLm11, Tdt+ thymoma, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 684)
Hahm, K., Ernst, P., Lo, K., Kim, G.S., Turck, C. and Smale, S.T. The lymphoid transcription factor LyF-1 is encoded by specific, alternatively spliced mRNAs derived from the Ikaros gene Mol. Cell. Biol. 14 (11), 7111-7123 (1994)
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/note="lymphoid transcription factor LyF-1 isoform VI"
                                                                                            253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 gitacaagcagagaagitcccitgaggagcacaaggagcgctgccgtacaittcitcaga 493
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                                                Gaps
                                                                                                                                        385 GTATTCGCCTGCCCAACGGGAAGCTCAAGTGTGATATCTGTGGGATAGTTTGCATTGGCC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenBank staff at the National Library of Medicine created thisentry (NCBI gibbsq 158967) from the original journal article. This sequence comes from Fig. 7A.
                                                                                                                                                                                      194 tcaatgtcttaatggttcataagcgaagccatactggtgaacgcccattccagtgtaatc
                                                                                                                                                                                                            GCGGTCACCTGCGTACCCCACTGTTGGAAAACCCCACAAGTGTGCTTACTGTGGGGCGGA
                                                                                                                                                                                                                                                                                                                                                                           agtgtgggggcatctttactcagaaaggtaacctcctccgccacattaaactgcacaca
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  Length 2301;
Score 204; . DB 4; Length 23
Pred. No. 1.9e-48;
0; Mismatches 125; Indels
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/organism="Mus sp."
/db_xref="taxon:10095"
4. .684
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  32.5%;
69.1%;
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                     Best Local Similarity 69.1
Matches 279; Conservative
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LRHIKLHSGEKPFKCHLCNYACRRRDALTGHLRTHSVGKPHKCGYCGRSYKQRSSLEE
HKERCHNYLQTMSISSNLYSVIKEETNQSEMAEDLCKIGSERSLVLDRLASNVARRKS
SMPQKFVGEKCLSDLPYDATINYEKENEIMQTHVIDQAINNAISYLGAESLRPLVQTP
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/db_xref="fD:g2330595"
/db_xref="G1:2330595"
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QSVKNERVLAGNNIETGYSDEENGRACEMNGESCAEDLRALDASGDKMGSHNGPGSK
AMSGVGGIRLPNGKLKCDICGIICIGPNVLMVHNRSHTGERPFQCNQCGASFTQKGNL
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SCQDSTDTESNNEERSGLIYLTNHIGPHARNGISVKEESRQFDVLRAGTDNSQDAFKV
I SSNGEQVRVYKCEHCRVLFLDHVMYTIHMGCHGFRDPFECNMCGYHSQDRYEFSSHI
                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 1557)
Liippo,J. and Lassila,O. Avian Itaros gene is expressed early in embryogenesis Eur. J. Immunol. 27 (8), 1853-1857 (1997)
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                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (12-MAR-1997) J.P. Liippo, Turku Immunology of Submitted (12-MAR-1997) J.P. Liippo, Turku University, Department of Medical Microbiology, Turku University, Ilinamyllynkatu 13, FIN-20520 Turku, FINLAND
Location/Qualifiers
1. 1557
/organism="Gallus"
/strain="RPD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Ikaros transcription factor"
/protein_id="CAA72531.1"
/db_xreff="PID:e309211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="thymus"
/cell_type="T lymphocyte"
/clone_lib="pCDM8 thymus cDNA"
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/germline
                                           Y11833.1 GI:2330594
Ikaros; transcription factor
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/gene="Ikaros"
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                                                                                                                 Gallus gallus
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                                                                                           chicken.
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Best Local Simi
Matches 338;
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                                                                                                                                                                                                                      /product="Ikaros homolog"
/product="Ikaros homolog"
/product="Ikaros homolog"
/product="10="AAAB97414."
/db_xref="PlD:g2062142"
/db_xref="PlD:g2062142"
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Karos/LyF-1; Ikaros/LyF-1 homolog"
/codon_start=1
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Pred. No. 5.8e-51;
0; Mismatches 152;
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                /db_xref="taxon:8022"
/cell_type="thymocyte"
1. .2496
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/strain="shasta"
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/gene="Ikaros"
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65.6%;
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/protein_id="AAG50459_1"
/db_xref="PID:131289371"
/db_xref="01:1289371"
/db_xref="01:1289371"
/translation="MDADEGODMSQVSGKESPPVSDTPDEGDEPMPTPEDLSTTSGGO_SSKSDRVVASNVKVETGSBENGRACEMORECAEDLRAMADASGEKNNGSHROGSS_ALSGVGGIRLPNGKKKSDIGGILGIGPNVLWYHKRSHTGERPPGCNGCGASTTOKGNL
LRHIKLHSGEKPFKCHLCNYACRRRDALTGHLRTHSVGKPHKCGYCGRSYKORSSLEE
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Submitted (10-NOV-1995) Wilfried Nietfeld, Department of Virology,
University of Freiburg, Institute for Medical Microbiology and
Hygiene, Hermann-Herder-Strasse 11, Freiburg 79104, Germany
Location/Qualifiers
1. 3629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to mouse LyF-1, encoded by GenBank
Accession Number S74708; similar to mouse Ikaros
DNA-binding protein, Swiss-Prot Accession Number Q03267"
/codon_starta.
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cds.
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ae; Homo.
ggacacattctgtggagaaaccctacaaatgtgagttttgtggaaggagttacaagcaga
                                                                                                                                                                                                                          1 others
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Human Ikaros/LyF-1 homolog (hIk-1) mRNA, complete
U40462
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Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 3629)
Nietfeld,W. and Meyerhans,A.
Cloning and sequencing of hIk-1, a cDNA enc
of mouse Ikaros/LyF-1
Immunol Lett. 49 (1-2), 139-141 (1996)
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/db_xref="taxon:9606"
/tissue_type="bone marrow"
169. .1728
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/gene="hik-1"
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Nietfeld, W.
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Oncorhynchus mykiss

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Protacanthopterygil;
Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 2496)
Hansen, J.D., Strassburger, P. and Du Pasquier, L.
Conservation of a master hematopoietic switch gene during
vertebrate evolution: isolation and characterization of Ikaros from
teleost and amphibian species
Eur. J. Immunol. 27 (11), 3049-3058 (1997)
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Oncorhynchus mykiss Ikaros homolog (Ikaros) mRNA, Ik-1 isoform,
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Direct Submission
Submitted (06-MAR-1997) Comparative Immunol., Basel Inst. for Immunology, Grenzacherstrasse 487, Basel CH-4005, Switzerland Location/Qualifiers
                                                                                                                                                                                                        326 ttaagtgtcacctctgcaactatgcatgccaaagaagaagatgcgctcacgggggcatctta
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                                             27;
Length 3629
Score 214.8; DB 11; Length
Pred. No. 1.5e-51;
0; Mismatches 137; Indels
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67.7%;
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LHAIKLHTGERFRCHLCAYAOQRADALTGHLEHTHYSPERYSYKESSSLEE
HKERCRAFLGAPDALGDAASVBARHIRAEMGSERALVLDRLASNVARKSSNEOKFIGE
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RCDHCHYLLLDYATHMGCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHRAMLK
399 c 399 g 290 t
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                              /note="Ikaros homolog; zinc finger transcription factor"
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il Similarity 88.1%; Pred. No. 1.9e-132;
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SMPQKFLGDKGLSDTPYDSATYEKENENMKSHYMDQAINNAINYLGAESELRPLVYOTPP
GGSEVVPVISPMYQLHRRSGTPRSHNSAQDSAYSLLLLJKKKLVPSEREASPSNSC
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TSGEQMKVYKCEHCRVLFLDHVMYTIHMGCHGFRDPFECNMCGYHSQDRYEFSSHITR
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ALSGVGGIRLPNGKLKCDICGIICIGPNVLMVHKRSHTGERPFQCNQCGASFTQKGNL
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                                                                                                                                                                                                                           Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 1788)
Mohlar, A., Wu,P., Largespada,D.A., Vortkamp,A., Scherer,S.,
Copeland,N.G., Jenkins, N.A., Bruns,G. and Georgopoulos,K.
The Ixaros gene encodes a family of lymphocyte-restricted zinc
finger DNA binding proteins, highly conserved in human and mouse
J. Immunol. 156 (2), 585-592 (1996)
S80876 1788 bp mRNA PRI 27-MAR-1997
IKAROS=hIK1 (alternatively spliced) (human, Jurkat T cell line,
mRNA Partial, 1788 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenBank staff at the National Library of Medicine created this entry (NCBI glubsq 177401) from the original journal article. This sequence comes from Fig. 1B and C. Map location: 7p13-p11.1.
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protein; This sequence comes
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/db_xref="taxon:9606"
238. 1788
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S80876 IKAROS=hIK1 U40462 Human IKaro U92201 Oncorhynchu Y11833 G.gallus mR U92198 Oncorhynchu S74708 IKaros/Lyr-AF044257 Mus muscu AF092175 Danio rer

S80876 HSU40462 OMU92201 GGIKTRF OMU92198 S74708 AF044257 AF092175

AB017615 Mus muscu 1092202 Xenopus lae 092202 Xenopus lae 092200 Oncorhynchu 092199 Oncorhynchu AF056116 Fugu rubr 132163 Homo saplen AF011573 Homo saplen AF011573 Homo saplen AF011573 Homo saplen AF01439 Xenopus l AF01439 Xenopus l AF01439 Xenopus l AF01439 Xenopus l AF014806 Homo saplen XF2553 Musculus D45210 Mouse mRNA U57796 Human Zinc U88080 Human Zinc U88080 Human Zinc U88080 Human Zinc 298745 Human DNA s AC005678 Homo sapl

> AF024439 HSA011806 HSOZF

AB017615 MUSIKAROS XLU92202 OMU92200 OMU92199 AF056116 HUMZIFI AF011573 G28565 MMU224805 MUSZFPAA HSU57796 HUMLD512P3

0110110110

AC005678 AC005822 AB007886

MMZFPR MMZFP35 MUSZFPB3

HSKOX1 HUMZNF8 AF020591

MMNZFP MMZFP37P1

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14.6 169931
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Copyright (c) 1993 - 1998 Compugen Ltd.
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Perfect score:
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X64413 M. musculus X17617 Mouse 2fp-3 M36146 Mouse 2inc X5233 Homo sapien M29581 Human zinc-AF020591 Homo sapi Y00850 Murine mRNA M15709 Mouse finge AL021918 Homo sapi X81804 B. taurus oz

X81804 B. taurus oz AC004262 Homo sapi AF045565 Mus muscu AC006116 Homo sapi AF153201 Homo sapi

HS34I8 BTOZFGENE

MUSFPB

AF045565 AC006116 AF153201 ALIGNMENTS

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AFO01293 AFO01293 1521 bp mRNA ROD 04-JUN-1997
LOCUS
DEFINITION MAS musculus transcription factor aiolos mRNA, partial cds.
ACCESION AFO01293
AFO01293. G1:2150043
AFO01293.1 G1:2150043
AFO01293.1 G1:2150043
AFO01293.1 G1:2150043
AFETWORDS
SOURCE
ONGANISM Musculus
Entheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Entheria: Rodentia; Sciurognathi; Muridae; Mus.
Entheria: Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS Morgan, B., Sun, L., Avitahl, N., Andrikopoulos, K., Ikeda, T.,
GONZales, E., Wu, P., Neben, S. and Goorgopouclos, K.
TITLE
Aiolos, a lymphod restricted transcription factor that interacts
JOURNAL EMBO J. 17, 2004-2013 (1997)
AUTHORS Morgan, B.
TITLE
DIRECT Submission
Charlestown, MA 02129, USA
LOCATION/Oualifiers
FEATURES
LOCATION/Oualifiers
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AF001293 Mus muscu

1521 12 AF001293

79.1

496.8

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Query Match Length DB

Score

Result No.

Description

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21;
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                                                                                                                                                                                                                                                                                                                                                                 202 -----ETSTKRSIK-----QNSNPVKKEKSCKCNECGKAFSYCSALIRHQRTHTGEKP 249
                                                                                                                                                                                                                                                                                                                                                                                                                             204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | : : | | : 370 TFTRSTHLTQHQKIHTGEKPY-----TYKCNECGKAFNGPSTFI--RHMIHTGEKPYECN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 --GYMYEKENEMMQ-----TRMMDQA-INNAISYLGAEAFRPLVQT--PPAPTSEMVP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 ECGRAFSQHSNLTQHQKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYRCNECGK 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 VISSVYPIALTRADMPMGAPQEMEKKRILLPEKILP-SERGLSPNNSAQDSTDTDSNHED 394
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522 KTHTQEKAYE-----YQCHE 562
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                                                                                                                                                                                                                                                                         145 FOCNOCGASFTOKGNLLRHIKLHTGEKPFKCHLCNYACORRDALTGHLRTHSVEKPYKCE
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                                                                                                                                                                                                      Indels 125;
                                                                                                                                                          Ouery Match 10.9%; Score 297.5; DB 4; Length 751; Best Local Similarity 22.6%; Pred. No. 5e-16; Matches 118; Conservative 78; Mismatches 201; Indels 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 CHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFSSH 496
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PFAM; PF01352; KRAB; 1.

PFAM; PF00096; zf-C2H2; 19.

PROSITE; PS00028; ZINC_FINGER_C2H2; 19.

SINC_finger; Metal-binding; DNA-binding.

SEQUENCE 751 AA; 86174 MW; C98BA039 CRC32;
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Search completed: November 6, 1999, 08:05:41

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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PHILLIPS S.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AL021918; CAA17278.1; -.
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Best Local Similarity
Matches 72; Conserva
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01-JUN-1998 (
01-MAY-1999 (
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043309
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80 IVHKRIHTGEKPYKCDICGKAFSYSSGLAVHKSIHPGKKAHECKDCGKSFSYNSLLLQHK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ERC----RAFLQNPDLGDAASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 FI--GEKRH-CFDANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 ISEMVPVISSVYPIALTRADMPMGAPQEMEKK----RILLPEKILPSERGLSPNNSAQDS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- 305
QHLYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPIC------LRDSIKVINKE 443
                 73 KPEPMGDAEESEMPYSYAREYSDYESIKLERHVPYDNSRPTSGKMNCDVCGLSCISFNVL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- QCNQCGASFTQKGNLLRHI 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-SKELETAL MUSCLE;
MEDLINE; 96404132.
MEDLINE; 96404132.
COSJUG., BOUCHE M.;
DIfferentiation dependent expression in muscle cells of ZT3, a nover finger factor differentially expressed in embryonic and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 RIHTGERPYKCEEC----GKAYIS-----LSSLINHKSVHPGEKPFK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 GEKPYKCSYCEKSFNYSSALEQHKRIHTR------EKPFGCDECGKAFRNNSGLKVHK
                                                          444 GEVMDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFSSH 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.9%; Score 298.5; DB 11; Length 623; 22.5%; Pred. No. 3.3e-16; Live 55; Mismatches 140; Indels 167;
                                                                                                                                                                                                                                                                                                 Mammalia;
Mus.
                                                                              RR----YECNECGKFFLDSYKLVIHQRIHTGEKPYKCSKCGKFFRYRCTLSRH
                                                                                                                                                                                                                                                                                                                                                                            BRADY J.P.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                            OI-MAY 1999 (Tramburel. 10, Last annotation update)
ZINC FINGER PROTEIN 62 (FRAGMENT).
ZEP62 OR ZEP OR ZT3.
Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata;
Eutheria: Rodentia: Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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PROSITE; PS00028; ZINC_FINGER_C2H2; 18.
Zinc-finger; Metal-binding; DNA-binding.
                                                                                                                                                                                                     Created)
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                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                    (TrEMBLrel.
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01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-EYE LENS;
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Matches 105; Conser
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ID 062510
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386 IDTDSNHEDRQHLYQQSHV--VLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKE 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 VKDEYSDRDENIM-KPEPMGDAEE----SEMPYSYARE----YSDYESIKLER---HVPY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISHIKAWA K., NAGASE T., NAKAJIMA D., SEKI N., OHIRA M., MIYAJIMA N., TANAKA A., KOTANI H., NOWURA N., OHARA O.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

EMBL: AB007886; BAA24856.11. -.

PFAM: PF00096; zf-C2H2; 10.

PROSTIE; PS000208; zINC_FINCER_C2H2; 9.

Zinc-finger: Metal-binding; DNN-binding.

SEQUENCE 604 AA; 70222 MW; C1A94D55 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 IQPTVELKSTEEQPLPTESPDALNDYSLP----KPHEIENVDSREAPANEDEDAGEDSMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                     344 -----FECDRCEKVFRNNSSLKVHKRIHTGEKPYECDICGKAYISH 384
                                                   ----NHK-KIHLGEKPYKCDVCEKSFNYTSLLSQHKRVHTREKP----
                                                                                                                                   444 GEVMDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCG--YRSH
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01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
B3418.1 (KRUPPEL RELATED ZINC FINGER PROTEIN 184).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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Pred. No. 3.8e-16;
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Best Local Similarity 24.29
Matches 100; Conservative
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01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----EDRQHLYQQ------SHVVLPQARNGMPLLKEVPRSFELLKPPP 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 GGPEARCKDCGKVFKYNHFLAIHQRSHTGERPFKCNECGKGFAQKHSLQVHTRMHTGERP
                                                                                        350 YTCTVCSKALTTKHSLLEHMSLHSGQKSFTCDQCGKYFSQNRQLKSHYRVHTGHSLPECK
                                                                                                                                                                                                                           -- DLGDAASVEARHIKAEMGSE------RALVLDRLASNVAKRKSSMPQKFIGEKRH
                                                                                                                                                                                                                                                                        GKSFSD-SSAKRRHCILHTGKKPFSCPECNLQFARLDNLKAHL------KIHSKEKH
                                                                                                                                                                                                                                                                                                                      280 CFDANYNPGYMYEKENE---MMQTRMMDQAINNAISYLGAEAFRPLVQTP-PAPTSEMVP
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1207 AA; 140376 MW; C54700DD CRC32;
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EMBL; 298745; CAB11428 1; -
FRAM; PF000969; Zf C-C2H2; 19.
PROSITE; PS00028; ZINC, FINGER, C2H2; 17.
Zinc-finger; Metal-binding; DNA-binding.
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Best Local Similarity
Matches 111; Conserv
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16;
                                                                                                                                      975 IHTRDKPYQCTQCNKSFSRRSILTQHQGVHTGAKPYECNECGKAFVYN-----SSL 1025
                                                                                                                                                                                                                                                                             ..----KECGKSFSQSG-----LIQHQRI 1058
                                                                                                                                                                                                                                                                                                                                                                                                                           1059 HTGEK-PYKCDVCEKAF-----IQRTSLTEHQRIHTGERPYKCDKCGKAFTQR 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1106 SVLTE-----HORIHT------GE--R 1119
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                                                                   ---KERCRAFLQNPDLGDAASVEARHIKAEMGSE-----RALVLDRLASNVAKRKSS 268
                                                                                                                                                                                                             MPQKFIGEKRHCFDANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPA 328
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RHK I IHTGEK PYKCNECGKAFGRWSALNQHQRLHTGEKHYHCNDCGKAFSQKAGLFHH IK
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LAMERDIN J.E., MCCREADY P.M., SKOWRONSKI E., ADAMSON A.W.,
BURKHART-SCHULTZ K., GORDON L., RYLE A., RAMIREZ M., STILMAGEN S.,
GARNES J., DANGANAN L., POUNDSTONE P., CHRISTENSEN M., GEORGESCU AVILA J., LIU S., BRUCE R., QUAN G., MONTGOMERY M., OW D., NOLAN PAVILA J., LIU S., BRUCE R., QUAN G., MONTGOMERY M., OW D., NOLAN B.
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO04076; AAB97932.1; -.
PRAM; PF00096; zf-CZH3: 16.
PRAM; PF00096; zl-CZH3: 16.
Zinc-finger; Metal-binding; Zinc-finger; Metal-binding.
SEQUENCE 691 AA; 80606 MW; 3FEAOBAF CRC32;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 VFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFSSH 496
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Last sequence update)
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24.2%; Pred. No. 2.18-1...
**ive 60; Mismatches 152;
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                                                                                                                                                                                                                                                              1026 VSHQEIHHKEKCYQC-------
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217 FSCISHHHDDNIVHKRDKVHSNSDCGKDTLKVSPLTQRSIHTGQKTYQGNECEEA---- 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 CISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 EESEPICEPSKEEEMPVEKD-----ENYD----PKTEDGQASQSRYSKR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SMKVKDEYSDRDENIMKPEPMGDAEESEMPYSYAREYSDYESIKLERHVPYDNSRP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEYSDRDENIMKPEPMGDAEESEMPYS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 TSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKP
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"Analysis of homologous XRCC1-linked zinc-finger gene families human and mouse: evidence for orthologous genes."; Genomics 49:112-121(1998).

EMBL, PRO275131, AAD1278-1; -.

PRAM; PF010512; KRAB; 1.

PRAM; PF01096; zf-C2H2; 8.

PROSTTE; PS00028; ZINC_FINGER_C2H2; 6.

Zinc_finger; Metal-binding; DNA-binding.

NON_TER 506

SEQUENCE 506 AA; 57498 MW; 7A530D9B CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                        Length 506;
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ISHIKAWA K., NACASE T., NAKAJIMA D., SEKI N., OHIRA M.,
TANAKA A., KOTANI H., NOMURA N., OHARA O.;
Submitted (COT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB007901; BAA23713.1; -.
PFAM; PF00651; BTB; 1.
PFAM; PF000058; ZI-C2H2; 8.
ZINC-finger; Metal-binding; DNA-binding.
SEQUENCE 697 AA; 78292 MW; 20075420 CRC32;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                     11.3%; Score 308; DB 4;
1larity 29.8%; Pred. No. 4.3e-17;
Conservative 33; Mismatches 86,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 DALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 TDLNIHCRVHTGEKPYKCEVCGKGFTQRSHLQAHE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269
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Best Local Similarity 22.0%;
Matches 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
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Best Local S
Matches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVPYDNSRPISGKM-----NCDVCGLSCISFNVLMVHKRSH-TGERPFQCNQCGASFTQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H------GKMKTYKCKQCDFIAVTKLSF---WEHNRIHIKPEKMLKCQKCPFITEY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEHKERCRAFLQNPDL-------GDAASVEARHIKAEMGSERALVLDRLA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLH----LRKYSHNPPMVLNYDGTPNPLRIIDVYGTRRGPKVKFHKDEGGH------NLLN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNVAKRKSSMPQKFIGEKRHCFDANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAF 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPLVQTPPAPTSEMVPVISSVYPIALTRADMPMGAPQEMEKKRILLPEK----ILPSER 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-LSPNNSAQDST-------DIDSNHEDRQHLYQQSHVVLPQARNG----MPLL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 GWQNEENCNEEETPEKEEDPKRMSALDLSSNPSTPSTVSQVKH----KRKGRAFKLELM 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 KEVP------WADVF 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Diptera; Nematocera; Psychodoidea; Psychodidae; Clogmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 485;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
ZINC FINGER PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%; Score 342.5; DB 5; 23.9%; Pred. No. 6.7e-20; iive 69; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Æ
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      Clogmia albipunctata (mothmidge)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 23.78 Matches 127; Conservative
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01-JAN-1998 (
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HANSEN J.D., STRASSBURGER P., DU PASQUIER L.;
"Conservation of a master hematopoietic switch gene during vertebrate evolution: isolation and characterization of Ikaros from teleost and amphibian species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 GERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKP 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Gaps
                                                                                                                                                                                            ALSO INTERACTS WITH A CRITICAL CONTROL ELEMENT IN THE TDT (TERMINAL DEDXINGLECOTIDYLTRANSFERASE) PROMOTER AS WELL AS WITH THE PROMOTERS FOR OTHER GENES EXPRESSED DURING EARLY STAGES OF IND T CELL DEVELOPMENT.
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MEDLINE: 96301401.
"Zfp-37 is a member of the KRAB zinc finger gene family and is expressed in neurons of the developing and adult CNS."; Genomics 33:247-257(1996).
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                                                                                                                                                                                                                                                                            -:- SUBCELLUAR LOCATION: NUCLEAR.
-:- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND SPLEEN.
NO EXPRESSION IN WISCLE.
-:- SIMILARITY: TO D. MELANOGASTER HUNCHBACK.
EMBL: U92202; AAB53435.1; -- PROSITE; PSO0028; ZINC-FINGER_C2H2; 3.
PROSITE; PSO00038; ZINC-FINGER_C2H2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein.
NON TER
SON_FING
SO
                                                                                 EUI. J. Immunol. 27:3049-3058(1997).
-!- FUNCTION: BINDS AND ACTIVATES THE ENHANCER
(DELTA-A ELEMENT) OF THE CD3-DELTA GENE.
FUNCTIONS IN THE SPECIFICATION AND THE MATURATION OF THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
20.0%; Score 546.5; DB 13; Length 138;
Best Local Similarity 73.2%; Pred. No. 4.8e-37;
Matches 101; Conservative 16; Mismatches 14; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 VLDRLASNVAKRKSSMPQ 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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RGOUENCE FROM N.A.

RC STRAIN=CBA/CA, CBA/C57BL, C57BL/6; TISSUE=BRAIN;

RM MEDLINE; 92310982.

RA BURKE P.S., WOLGEMUTH D.J.;

RT Tafp-37, a new mutine tinc finger encoding gene, is expressed in a developmentally requilated pattern in the male germ line.";

RL Nucleic Acids Res. 20:2827-2834(1992).

BR FAM; PF001352; KRAB; I.

DR PFAM; PF001352; KRAB; I.

DR PFAM; PF000056; zf-C242; 12.

DR PROSITE; PS00028; ZINC_FINGER_C2H2; 11.

KW Zinc-finger; Metal-binding; DNA-binding;
FT CONFLICT 300 300 L -> V (IN REF. 3).

FT CONFLICT 528 528 T -> P (IN REF. 3).

FT CONFLICT 572 572 F -> V (IN REF. 2).

FT CONFLICT 572 F -> V (IN REF. 2).

FT CONFLICT 572 F -> V (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 ALTGHLRIHSVEKPYKCEFCGRSYKQRSSLEEH-------KERCRAFLQNPDLGD 234
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Best Local Similarity 23.3%; Pred. No. 5.5e-20;
Matches 114; Conservative 55; Mismatches 129; Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 594;
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Last annotation update)
Nucleic Acids Res. 18:3655-3655(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 VEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCFDANYNPGYMYEKENEM 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVYPIALTRADMPMGAPQE 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota: Mettacoa: Chordata; Craniata: Vertebrata: Actinopterygli;
Neopterygli: Teleostei: Euteleostei: Acanthopterygli; Percomorpha:
Tetraodontiformes; Tetraodontoldei: Tetraodontidae: Fugu.
                                                                                              PGPSKEVLRVVGESGEPVKAFKCEHCRILFLDHVMFTIHMGCHGFRDPFECNICGYHSQD
                                                        PICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
GELLNER K., BRENNER S.;
GELLNER K., BRENNER S.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
BMBL, AF056116; AAC34387.1; -.
PFAM: PF00006; zf-c2Hz; 5.
PROSITE; PS00028; ZINC_FINGER_C2H2; 5.
Zinc-finger; Metal-binding; DNA-binding.
SEQUENCE 417 AA: 45664 MW; 7856E12F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
IKAROS-LIKE.
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Pred. No. 3e-62.
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37.2%;
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Matches 193; Conservative
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                                                                                                                                                                                   RYEFSSHIARGEHR 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKFIGEK -- RHCF-DANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APTSEMVPVISSVYPIAL - - TRADMPMGA - - - - - PQEMEKKRILLPEKILPSERGLSPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 NSAQDSTDTDSNHEDRQHLYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKV
042244 PRELIMINARY: PRT; 328 AA.
042244;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1999 (TrEMBLrel. 05, Last sequence update)
01-JAN-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TRANSCRIPTION FACTOR (FRAGMENT).
Xenopus laevis (African clawed frog).
EUKATYOTA: Metazoa: Chordata; Craniata: Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYF-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKAROS OR LYF-1.
Xenopus laevisygilli.
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 328;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA-BINDING PROTEIN IKAROS (LYMPHOID TRANSCRIPTION F
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.0%; Score 681.5; DB 13;
44.4%; Pred. No. 1.9e-47;
Live 55; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                     328 AA; 37116 MW; CCC9E71E CRC32;
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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

TURPEN J., KELLEY C., MEAD P., ZON L.;

TURNULLY 0:0-0(1997).

EMBL; AFOZ4439; AAB81280.1; -.

PFAM; PF00096; zf-CZH2; 2.

PROSITE; PS00028; ZINC_FINGER_CZH2; 2.

Zinc_finger; Metal-binding; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 INKEGEVMDVFRCDHCHVLFLDYVMFTIHMG 470
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013100;
01-AUG-1998 (TrEMBLrel.
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Best Local Similarity
Matches 147; Conserv
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01-MAY-1999 (TrEMBLrel. 10
01-MAY-1999 (TrEMBLrel. 10
EOS PROTEIN.
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                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                (Mouse).
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SEQUENCE FROM N.A.
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|ITRGEHR 536
                                                        497 IARGEHR 503
                                                                                                                                                                                                musculus
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                                                                                                                                                                                                                                                                             WANAKA A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKERCRAFLQNPDLGDAA-SVEARHIKAEM----GSERALVLDRLASNVAKRKSSMPQK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVPVISSVYPIALTRADMPMGAPQEMEKKRILLPEKILPSERGLSPNNSAQDSTDTDSNH 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                              8 EMSQITGRDSPMNANE-GGEDQDEAMPVPEDLSASTGLQHNNRTDKPLACNIKVEARSDE 66
                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Actinopterygii;
Neopterygii: Teleostei: Euteleostei; Ostariophysi: Cypriniformes;
[1]
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KRILLPEKILPSERGLSPNNSAQDSTDTDSNHEDRQHLYQQSHVVLPQARNGMPLLKEVP
                                     RSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFEC
                                                                                                                                                                                                                                                                                                                                                                                      Length 537;
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                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                       AMENOTA C., KAWASAKI H.;
"Characterization of zebrafish ikaros, a gene necessary
differentiation of the immune system.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF092175; AAC61763.1; -.
PROMITE PF000058; zI-CZH2; 5.
PROSITE; PS000058; zINC_FINGER_CZH2; 5.
ZINC_FINGER: Metal-binding; DNA-binding.
SEQUENCE 537 AA; 58865 MW; 6AF8330F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                    42.7%; Score 1165.5; DB 13;
45.7%; Pred. No. 3.2e-86;
Live 66; Mismatches 134; Ir
                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                              PRELIMINARY;
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Best Local Simi
Matches 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                   DSTDTDSNHEDRQHLYQQSHVVLPQA------RNGMPLLKEVPRSFE-LLKPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 KSTEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVK---DEYSDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 TPVISSVYTQMQPIP-SRLELPGSREAGEGPEDLGDGGPLLYRARGSLTDPGASPSNGCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMMA Y., KIYOSAWA H., MORI T., OGURI A., NIKAIDO T., KANAZAWA TOJO M., TAKEDA J., TANNO Y., YOKOYA S., KAWABATA I., IKEDA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Bos: a novel member of the Ikaros gene family expressed predominantly in the developing nervous system."; FEBS Lett. 0:0-0(1999).
EMBL; AB017615; BAA36213.1; -.
EMBL; AB017615; BAA36213.1; -.
Zinc-finger; PS00028; ZINC_FINGER_C212; 5.
Zinc-finger; ABA1-binding; DRA-binding.
SEQUENCE 5:3 AA1-binding; AA0315AD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.0%; Score 1090; DB 11
44.0%; Pred. No. 3.9e-80;
                                                                                                                                                                                                                                                                 Æ
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                                                                                                                                                                                                                                                                 533
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                                                                                                                                                                                                                                                                                                  10,
10,
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18;

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein - protein search, using sw model

November 6, 1999, 06:57:53 ; Search time 24.57 Seconds (without alignments) 1269.948 Million cell updates/sec US-09-019-348-2 2728 1 MEDIQPIVELKSTEEQPLPT......HDRYEFSSHIARGEHRAMLK 507 Title: Perfect score: Sequence: Run on:

201082 segs, 61543640 residues Searched:

BLOSUM62

Scoring table:

SPTREMBL_10:* Database :

sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_nwertebrate:*
sp_mammal:*
sp_mammal:*
sp_nganelle:*
sp_phage:*
sp_phage:*
sp_plage:*
sp_vlrus:*
sp_vrrushate:*
sp_vrrushate:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O08900 mus musculu	093581 brachydanio	Q9z2z2 mus musculu	P79751 fugu rubrip	042244 xenopus lae	013100 xenopus lae	Q62514 mus musculu	. 096785 clogmia alb		O43167 homo sapien	рошо	рошо		O43309 homo sapien	O60792 homo sapien	P70590 rattus norv	Q62512 mus musculu	Q62886 rattus norv	Q14588 homo sapien	O88412 mus musculu	8 mus	Q15917 homo sapien	рошо	Q15776 homo sapien	O35483 mus musculu	homod	homo	Q13398 homo sapien	Q61491 mus musculu
SUMMAKTES	. QI	008800	093581	092222	P79751	042244	013100	062514	096785	014898	043167	043724	043361	062510	043309	060792	P70590	062512	062886	Q14588	088412	09Z1D8	015917	092951	015776	035483	075802	015361	Q13398	061491
	DB	11	13	11	13	13		11	Ŋ	4	4	4	4	11	4	4	11	11	11	4	11	11	4	4	4	11	4	4	4	11
	Length	507		533	417	328	138	594	485	206	697	1207	691	623	604	751	. 591	346	650	693	524	819	622	273	578	812	612	394	367	546
ф	Query	100.0	CA.	•	31.8	25.0	20.0	12.6	12.6	11.3	11.2	11.1	11.1	10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.7	10.6	10.6	10.6	10.6
	Score	2728	1165.5	1090	866.5	681.5	546.5	345	342.5	308	306	302.5	301.5	298.5	297.5	297.5	296.5	296.5	295.5	295	294.5	294.5	292	262	. 291	29	289.5	œ	8	288
	Result No.	П	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

O43345 homo sapien Q920q5 mus musculu	OO8961 rattus norv O14709 homo sapien	014593 homo sapien 000455 homo sapien	Q02313 homo sapien Q09046 xenopus lae	O75701 homo sapien Q9z117 mus musculu	O70162 mus musculu O95201 homo sapien	O88553 rattus norv	043693 homo sapien	D D D D	095015 homo sapien
1 043345 11 Q920Q5	11 008961 1 014709	1 Q14593 1 O00455	1 002313 13 009046		11 070162 4 095201			014586	095015
1167	1186	385	591				-	/32	430
10.5	10.5	10.4	10.4	10.4 10.4	10.3	10.3	10.3	10.2	10.2
286.5	285.5 284.5	284.5	283.5 283.5	283 283	281.5 281	281	280.5	57.9	278.5
30 31	332	34 35	36 37	338	4 0	42	43	44	45

ALIGNMENTS

PRI; 507 AA. Created)	IL N., ANDRIKOPOULOS K., IKEDA T., 1 S., GEORGOPOULOS K.; Licted transcription factor that interacts ymphocyte differentiation.";); 1.	MW; 8E23A71B CRC32; 0%; Score 2728; DB 11; Length 507; 0%; Pred. No. 2.8e-212; 0; Mismatches 0; Indels 0; Gaps	ESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKV 60 	EESEMPYSYAREYSDYESIKLERHVPYDNSRPTSGKMNCD 120 	VCGLSCISFNVLMVHRRSHIGERPFOCNOCGASFIOKCNLLRHIKLHTGEKPFKCHLCNY 180 	YYKCEFCGRSYKORSSLEEHKERCRAFLQNPDLGDAASVEA 240	RHIKAEMGSERALVLDRLASNVAKRKSSMPOKFIGEKRHCFDANYNPGYMYEKENEMMOT 300 	RWMDQAINNAISYLGAEAFRPLVQTPPAPTSEWVPVISSVYPIALTRADMPMGAPQEMEK 360
		L N., ANDRIKOPOULOS K., IKEDA T., S., GEORGOPOULOS K.; icted transcription factor that interacts ymphocyte differentiation.";);	A T., hat interac	A T., hat interac ngth 507; els 0; EDEDAGEDSMK	GEORGOPOULOS K., IKEDA T., GEORGOPOULOS K.; d transcription factor that interacts ocyte differentiation."; BE23A71B CRC32; Score 2728; DB 11; Length 507; Pred. No. 2.8e-212; Mismatches 0; Indels 0; Ga ALNDYSLEWPHEIENVOSREAPANEDEDAGEDSMKV H	A T., hat interacts hat interacts els 0; Ga EDEDAGEDSMKV	A T., hat interacts ngth 507; els 0; Ga EDEDAGEDSMKV	A T., hat interacts hat interacts ngth 507; els 0; Ga EDEDAGEDSMKV IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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                                                                                                                                                                                                                                                                                       RSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHS 196
                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAŽOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                    46 PANEDEDAGEDSMKVKDEYSDRDENIM---KPEPMGDAEESEMPYSYAREYSDYE---SI 99
                                                                                                                                                                             Gaps
                                                                                                                                                                                                12 STEEQPLPTESP-----VDSREA 45
                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 90040698.
NIETFELD W., EL-BARADI T., MENTZEL H., PIELER T., KOESTER M.,
                                                                                                                                                        Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POETING A., KNOECHEL W.; Second-order repeats in Xenopus laevis finger proteins."; J. MOL. BIOL. 208:639-659(1989).
PIR; S06556; S06556.
PROSITE; PS00028; ZINC_FINGER_C2H2; 13.
PFAM: PF00096; Zf-C2H2; 13.
HSSP; P08047; 1SP2.
          DNA-BINDING; METAL-BINDING; NUCLEAR PROTEIN.
                                                                                                                                                                            Indels
                                                                                                                                                        10.9%; Score 298.5; DB 1; 29.9%; Pred. No. 1.5e-13;
                             BOX").
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT.
                                                                                                                            F98854DC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
OOCYTE ZINC FINGER PROTEIN XLCOF28 (FRAGMENT)
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
                                                                                                                                                                                                                                                                                                                                                                                                                            439 AA
                                                                                                                                                                            40; Mismatches
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KRAB BOX ("B B

ZINC-FINGERS.

C2H2-TYPE.

C2H2-TYPE.

C2H2-TYPE.

C2H2-TYPE.

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C2H2-TYPE.
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C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                       197 VEKPYKCEFCGRSYKQRSSLEEHK 220
                                                                                                                                                                                                                                                                                                                                                                   305 GEKPYECQDCGRAFNQNSSLGRHK 328
                                                                                                                                                                                                                                                                                                                                                                                                                         2028_XENLA STANDARD;
P18747;
01-NOV-1990 (REL. 16, CREATED)
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                                                                                                                            61772
                                                                                                                                                                  Best Local Similarity 29.9
Matches 79; Conservative
HSSP; P08047; 1SP2
        ZINC-FINGER;
                                                                                              ZN_FING
ZN_FING
ZN_FING
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                                                                                                                                                                                                                                                                                                                               156 QKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSS 215
                                                                                                                                                                                                                                                                                                                                                                                                            216 LEEHKERCRAFLQNPDLGDAASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                   259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 EKRHCFDANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQHL--YQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVIN--KEGEVMD-- 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 KSKLVVHQRTHT-------GERPFKC----SVCDKTFIRMVHLLEHRKIHDGD 386
                                                                                                                                                                                                                                                                         336 VISSVYPIALTRADMPMGAPQEMEKKRILLPEKILPSERGL-SPNNSAQDSTDTDSNHED 394
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                      DSPNCEKT-----FEQES-APKTATMDQLHESA-------GLEKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 EL----PEATNSVESP-EAIDDYEKNYI--PWSPLSEYLGVFLPPEKQHKCTECDKCFLE
                                                                                                                                                                       10.9%; Score 29%; DB 1; Length 439; 24.7%; Pred. No. 1.3e-13; Live 53; Mismatches 136; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -VFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCG 484
                                                                                                                 57799C28 CRC32;
                                    C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
  C2H2-TYPE.
C2H2-TYPE.
                                                                                                                 MM.
252
355
383
411
439
51350 1
                                                                                                                                                                 Query Match
Best Local Similarity 24.7%
Matches 98; Conservative
230
333
361
389
417
439
439 AA;
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Search completed: November 6, 1999, 11:46:20 Job time: 6524 sec

259 337 295 396 342 448 392

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEFAMKSNLLVHYSVHSGERPFSCTECDKTFSNKAQLEKHLRVHTGERPYSCEQCGKSFA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                            393 STHISPSTEFGVQTTEDNHQSPSKDHTGEKPFSCSECGKSFFYKSVLKDHLVVHTGKKPY 452
                                                                       281 FDANYNPGYMYEKENEMM---QTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVI
                                                                                                                                                                                                                                                                                      RRDALIGHLRIHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNPDLGDAASVEARHI
                                                                                                                                                                                                                                 -- KPFPCTKCWGIF
                                                                                                                                                                                                                                                                  338 SSVYPIALTRADMPMGAPQEMEKKRILLPEKILPS-ERGLSPNNSAQDSTDTDSNHEDRQ
                                                                                                                                                                                                                                                                                                                                      HLYQQSHVVLPQAR-----NGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVM---
                                                                                                                                                                                                                                                                                                                                                                                                          -----THMGCHGERDPE
                                                                                                                        244 KAEMG---SERALVLDRL--------ASNVAKRKSSMPQKFIGEKR--HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANOTATION UPDATE)
ZINC FINGER PROTEIN 8 (ZINC FINGER PROTEIN HF.18) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 AA.
                                                                                                                                                                                                                             260 TEC----GEIFSNEHELLTHQSTHTEEQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00028; ZINC_FINGER_C2H2; 7. PFAM; PF00096; zf-C2H2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 HCIECGRSYTHQSSLKSHQR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 ECNMCG-----YRSHDR 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M29581; G340448; -. PIR; B34612; B34612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 90169993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZNO8_HUMAN
ID ZNO8_HUMAN
AC P17098;
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                                                                                                                                                                                                                                                                                                                                      397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                  EUKRRYOTE, METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 LSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQ 183
                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE; 95094815.
SCHABEFER U., RAUSCH O., BOUWMEESTER T., PIELER T.;
"Sequence-specific recognition of a repetitive DNA element by a C2H2 zinc-finger protein in Xenopus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 EEQPLPTESPDALNDYSLPK-----PHEIENVDSREAPANEDEDAGEDSMKVKDEY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEEP-----YEFPENTFGINELLPNYQQNCTDGEAISDIKSDLAYLEVEITDAH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 -- EESNTDKPFTC----TECGKTFTRK-PNYES----HIRAHKGEKPFS----CMVCD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 175;
                                                                                                                                                                                                                                                                                                                              MEDILINE: 90040698.
NIETFELD W., EL-BARADI T., MENTZEL H., PIELER T., KOESTER M., POETING A., KNOECHEL W., Second-order repeats in Xenopus laevis finger proteins."; J. MOL. BIOL. 208:639-659(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 299.5; DB 1; Length 675; 21.2%; Pred. No. 1.7e-13;
                                                                 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
GASTRULA ZINC FINGER PROTEIN XFG20-1 (XLCGF20.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2H2-TYPE.
3468F756 CRC32;
                675 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC2H2-TYPE.
CC2H2-TYPE.
CC2H2-TYPE.
CC2H2-TYPE.
CC2H2-TYPE.
CC2H2-TYPE.
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CC2H2-TYPE.
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PIR; S06565; S06565.
PROSLITE: PS00028; ZINC_FINGER_C2H2; 17.
PFAM: PF00096; Zf-C2H2; 18.
HSSP; P25490; 1ZNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2H2-TYPE
                                                                                                                       XENOPUS LAEVIS (AFRICAN CLAWED FROG)
                  PRT;
                                                                                                                                                                                                                                                                                 EUR. J. BIOCHEM. 226:567-576(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
                                               01-NOV-1990 (REL. 16, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77116 MW;
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 85-613 FROM N.A.
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                STANDARD;
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619
675 AA;
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424
452
507
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01-OCT-1996
              ZG20_XENLA
P18714;
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ZN_FING
SEQUENCE
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Matches 11
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                                                      20;
                                                                                                                                                                                                                                                                                                                                            RKLCLSHLQKGDKGEKHFECNECGKAFWEKSHLTRHQRVHTGQKPFQCNECEKAFWDKSN 408
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MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
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                                                      Gaps
                                                                                                     ENVDSREAPANEDEDAGEDSMKVKD---EYSDRDENIMK----PEPMGDAEESEMPYS- 89
                                                                                                                                    -NCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGN
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                                                      Indels 141;
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"Second-order repeats in Xenopus laevis finger proteins.";
J. MOL. BIOL. 208:639-659(1989).
     Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNOCHEL W., POTING A., KOSTER M., EL BARADI T., NIETFELD W., BOUWMEESTER T., PIELER T.; "Evolutionary conserved modules associated with zinc fingers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
GASTROLLA ZINC FINGER PROTEIN XLCGF48.2 (FRAGMENT).
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEKPYECHECGKIFYNKSY ------LTKHNRTHTGEKP-
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  11.1%; Score 302.5; DB 1; 22.5%; Pred. No. 1.4e-13; ive 74; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROC. NATL. ACAD. SCI. U.S.A. 86:6097-6100(1989)
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Query Match
Best Local Similarity 22.59
Matches 117; Conservative
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P18723;
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agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKE---- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 EPFVCSECGKSFAQSPQLD-----LHMRIHTGEKPFSCSDCGKCFTQRADLNVHRRTH 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKTIKEEPDSCEE-EKLSDYKIITVSE------PVAEDQNPAPSCSQNNRSLPNYVS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIMKPEPMGDAEESEMPYSYAREYSDYESIKL.....-ERHVPYDNSRPT.-- 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 302.5; DB 1;
Pred. No. 9.9e-14;
3; Mismatches 186;
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entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                          PIR; F33282; F33282.
PIR; S06573; S06573; S06573; S06573; PROSITE; PS00028; ZINC_FINGER_C2H2; PFAM; PFO0096; Zf-C2H2; 12.
HSSP; P08047; LSP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM;
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                                                                                                                                                                            METAL-BINDING;
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                                                         EMBL; M25871; G214967;
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Best Local Similarity
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                                                                                                                                                                          ZINC-FINGER;
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REGULATION; NUCLEAR PROTEIN; SPERMATOGENESIS;

RANSCRIPTION

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29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385
                                                                                                                                                                                                                                                                                           78 YNCDECDQSFAWSTGLIRHQRTHWKPYECEEGGKAFRMSSALVLHQRIHTGEKPYPCSWC 137
                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                    KCEFCGRSYKQRSSLEEHKE------RC-RAFLQNPDLGDAASVEARHIKAEMGS 249
                                                                                                                                                                                                                                                                                                                                                                                                         ERALVLDRLASNVAKRKSSMPQKFIGEKRHCFDANYNPGYMYEKENEMMQTRMMDQAINN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                          310 AISYLGAEAFRPLVQTPPAPTSEMVPVISSVYPIALTRADMPM------GAPQEMEK-- 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 KTFSOSSNLILHQRIHTGEKPYPCNSCSKSFSRGSDLIKHQRVHTGEKPYTCNLCSKSFS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDIDSNHEDROH-------LYQQSHVVL-----PQARNGMPLLKEVPRS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F----ELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPF 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSQKSDLIKHQRI------HTGE--KPYKC-MCGKAFSQCSAFTLHQRIHTGEKPY 551
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                           EPATEEEMTGKIGTVTEESGSLEE---DVPH-----DSRGKEFREFGEELNDQMLFRRRQ 77
                                                                                                                                                                                                                                                                                                                                                   K-----PYKCSECGKAFNQSSVLILHQRIHTGEKPY-PCNQCTKS----FSRLSD-LINH
                                                                                                                                                                                                                                                                                                           --SYAREYSDYESIKLER----HVPYDNSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTG
                                                                                                                                                                                                                                                                                                                                                                                    65 SDRDE-----EESEMPY---EPMGDA-------EESEMPY----
                                                                                                                                                                                                                                                                                                                                           ERPFOCNOCGASFTOKGNLLRHIKLHTGEKPFKCHLCNYACORRDALTGHLRTHSVEKPY
                                                                                                                                                                                                                                            QPTVELKSTEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 OSSDLTKHORVHSGEKPYHCSSCNKAFROSSDLILHHRVHTGERPYA-----CTQCPRS
                                                                                                                                                                                                                             Mismatches 204; Indels 200;
                                                                                                                                                                                                             Length 580;
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452E3C1A CRC32;
                                                                                                                                                                                                            Score 307; DB 1;
Pred. No. 4.2e-14;
               ASP/GLU-RICH (ZINC-FINGERS. C2H2-TYPE.
                                      C2H2-TYPE.
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ilarity 22.5%; Pre
Conservative 75;
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        FACTOR;
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Best Local Similarity
Matches 139; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primate evolution.";
NUCLEIC ACIDS RES. 21:1409-1417(1993).
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-
FINGER PROTEINS.
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TUNNACLIFFE A., LIU L., MOORE J.K., LEVERSHA M.A., JACKSON M.S., FERGUSON-SMITH M.A., THIESEN H.-J., PONDER B.A.;
"Duplicated KOX zinc finger gene clusters flank the centromere of human chromosome 10: evidence for a pericentric inversion during
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE, 96051398
NOMURA N., NAGASE T., MIYAJIMA N., SAZUKA T., TANAKA A., SATO S.,
SEKI N., KAWARABAYASI Y., ISHIKAWA K. I., TABATA S.;
"Prediction of the coding sequences of unidentified human genes."
The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced banalysis of coha clones from human cell line KG-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR PROTEIN; REPEAT
                                                         ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRA3GENT).
ZNF33A OR ZENSAGENT).
HOMO SAPTRNE ''''''
                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC32;
848 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZINC-FINGER; DNA-BINDING; METAL-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C2H2-TYPE.
226A5F84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00028; ZINC_FINGER_C2H2; 16. PFAM; PF00096; Zf-C2H2; 16. HSSP; P08045; 1ZNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C2H2-TYPE.
    PRT;
                                            34, CREATED)
35, LAST SEQ
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98528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D31763; G498152; -. EMBL; X68687; G829150; -. EMBL; X68689; G296455; -.
    STANDARD;
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Q06730;
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----XOSNNFST----
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STRAIN-MF1; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 9:197-205(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X17617; G55473;
                                                                                                                                                                                                                                                                                                                                                                   MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A37107; A37107
PIR; S07667; S07667
MGD; MGI:99179; ZFP
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-MF1; TISSUE:
MEDLINE; 90107944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spermatogenesis
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                                                                                                                                                                                                                                                                             ZF35_MOUSE
P15620;
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                                                                                                                                                                                                                                                      RESULT 10
ZF35_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
repressor protein with differential DNa-binding domains.";

DNA CELL BIOL. 14:971-981(1995).

- FUNCTION: MAY FUNCTION AS A REPRESSOR OR SILENCER. PROTEIN, AND MOST LIKELY EXERTS ITS REPRESSING ACTIVITY UPON ZINC-DEPENDENT BINDING TO DNA. MAY BE INVOLVED IN PROPER SPERMATOGENESIS BY REPRESSING THE EXPRESSION OF GENES UNNECESSARY OR INCOMPATIBLE WITH THE MAINTENANCE OF A HAPLOID CELL STATE.

- SUBCELLULAR LOCATION: NUCLEAR.

- SUBCELLULAR LOCATION: NUCLEAR.

- TISSUE SPECIFICITY: BRAIN, HEART, SPLEEN, THYMUS, AND TESTIS.

- TISSUE SPECIFICITY: BRAIN, HEART SPEEN, THYMUS, AND TESTIS.

- TAGES 18-20 (SIMULTANEOUSLY TO THE APPEARANCE OF HAPLOID CELL STAGES. MAXIMAL EXPRESSION IS OBSERVED AROUND 2 WEEKS POSTUMATALLY, WITH THE EXCEPTION OF BRAIN AND TESTIS, WHERE THE EXPRESSION IS HIGHEST IN EARLIER DEVELOPMENTAL STAGES.

- SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQNKVGEDSSLSTDLVPQLDISSSIRPSDCKTFGNNLEHNSELVTQSNILAKKKPYKCDK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SYAREYSDYESIKLERHVPYDNSR---PTSGKMN--CDVCGLSCISFNVLMVHKRSH 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----RAFLQNPDLGDAASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRH 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDEDAGEDSMKVKDEYSDRD-ENIMKP---EPMGDAEE--SEM------PY---- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 CRKSFIHRSSLNKHEKIHKGDPYSNGTDQGAQSGRKHHECADCGKTFLWRTQLTEHQRIH
                                                                                                                                                                                                                                                                                                                                                                                            DNA-BINDING; NUCLEAR PROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 636;
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                                                                                                                                                                                                                                                                                                                                                                                                                   BOX").
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2H2-TYPE.
789C5355 CRC32;
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C2H2-TYPE.
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C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                        MGD; MGI:104786; ZFP90.
PROSITE; PS00028; ZINC_FINGER_C2H2; 13.
PFAM; PF00096; Zf-C2H2; 13.
HSSP: P08047; 1SP2.
                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 KRAB BOX.
                                                                                                                                                                                                                                                                                                                                                                                           ZINC-FINGER; METAL-BINDING; DNA-BIN
TRANSCRIPTION REGULATION; REPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                   KRAB 1
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606
636 AA;
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Matches 116; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                280 CFDANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISS 339
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                                                                                                                                                                                                                                                                                                                                                                                                          399 YQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----YQCNVCGKA
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"Genomic analysis of a mouse zinc finger gene, 2fp-35, that is up-
                                                                                                                                                                                                                                             340 VYPIALTRADMPMGAPQEMEKKRILLPEKILPSERGLSPNNSAQD-STDTDSNHEDRQHL
                                                                                                                                                                                                                                                                                                                         ------LPQG-----EGLLTEVKSYHCNDCGKDFGHITDFSEHQRLHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUNLIFFE V.T., KOOPMAN P., MCLAREN A., TROWSDALE J.; "A mouse zinc finger gene which is transiently expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC-FINGER; METAL-BINDING; DNA-BINDING; DEVELOPMENTAL PROTEIN;
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                            ----AFVP--NTP-
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01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
11C FINGER PROTEIN 35 (ZEP-35).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           580 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      470 GENSY-----GSEQTLLGOOSLSHPREKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulated during spermatogenesis."; GENOMICS 8:331-339(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503 FKRSTSFIEHHRIHTGEKPYECNECG 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 FLDYVMFTIHMGCHGFRDPFECNMCG 484
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393 SICGRAFGQSPSL-----YKHMRI--
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200 KIFKCKQCDFVAITKLEQWNHSKVHIRE----DKRLTCPKCPFITEYKHHLEYHLRNHAGS 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 KISEHSVDELSGKSDN------DAEE---------YDEQSLR----VPKVNSHGKI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 GKMNCDVCGLSCIS----FNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 EPLVSPKSEKEEKDMETTLTPCASPNRKPD------DNQDHLRRLEMSLEKSGLFSS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 KVK----DEYSDRDENIMKPEPMGDAEESEMPYSYAREYSDYESIKLERHVPYDNSRPTS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 QPTVELKSTEEQP-----LPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSM 58
   ZINC-FINGER; METAL-BINDING; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 YE----KENEMMQTR-MMDQAINNAISYLGAEAFRPLVQTP---PAPTSEMVPVISSVYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 IDVHGTRRGPKIKTQPKAEEAKPETLPFLNLQQQLPFPGYPFFGGFPNAQLLQQL----
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MEDLINE; 96089544.
LANGE R., CHRISTOPH A., THIESEN H.-J., VOPPER G., JOHNSON K.R.,
LEANGE R., PLOMANN M., CREMER H., BARTHELS D., HEINLEIN U.A.O.;
"Developmentally regulated mouse gene NK10 encodes a zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                   66; Mismatches 192; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                           Length 524;
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Q61967;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
2INC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).
ZFP90 OR NK10.
MUS MUSGCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERI
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Pred. No. 2.3e-14;
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ZINC-FINGERS I
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                               PROTEIN.
      DEVELOPMENTAL PROTEIN;
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                           REPEAT; NUCLEAR
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ZF90_MOUSE
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TGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERGLSPNNSAQDSTDTDSNHE---DRQHLYQQSHVVLPQARNGMPLLKEVPRSFELL-- 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 ERPYQCAECHKGFIQKSDLVKHLRTHTGEKPFKCSHCDKKFTERSALAKHQRTHTGEKPY 438
                               PYKCEFCGRSYKQRSSLEEHKERCRAFLQNPDLGDAASVEARHIKAEMGS---ERALVLD
                                                                                                                                                                              ------FIQNSDL-----VKHLRTHTGEKPYECPLCVK
                                                                                                                                                                                                                                            RLASNVA----KRKSSMPQKF-IGEKRHCFDANYNPGYMYEKENEMMQTRMMDQAINNAI
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                                                                                                                                                                                                                                                                                                RFAESSALMKHKRTHSTHRPFRCSECSRSFTHNSDLTAHMRKHTEFRNVLNLDS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                       310 ------KIFKRWKSFL-----
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MEDLINE; 96125163.
WOLFF C., SOMMER R., SCHRODER R., GLASER G., TAUTZ D.;
"Conserved and divergent expression aspects of the Drosophila segmentation gene hunchback in the short germ band embryo of the flour beetle Tribolium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HB.
TRIBOLIUM CASTANEUM (RED FLOUR BEETLE).
EUKARYOTA: METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA: COLEOPTERA; POLYPHAGA; CUCUJIFORMIA; TENEBRIONIDAE;
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LAST SEQUENCE UPDATE)
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EMBL; L01615; G161662; -
PROSITE; PSGO0028; ZINC_FINGER_C2H2; 3.
PFAM: PF00096; zf-C2H2; 6.
HSSP; P08151; 2GLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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01-OCT-1996
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Q01791;
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                                                                                                                                                                                                                                                                                                                                                                                               XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
 LLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHMGCHGF 474
                                                                                           -----YKCDECGKAFGHSSSLTYHMRTHTG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
MEDLINE; 94021366.
ANDREAZZOLI M., DE LUCCHINI S., COSTA M., BARSACCHI G.;
"RNA binding properties and evolutionary conservation of the Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBRYOGENESIS.

DOMAIN: CONTAINS 37 FINGER MOTIFS IN 6 DOMAINS.

PTM: PHOSPHORYLAYED.

SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEE M.S., GIPPERT G.P., SOMAN K.V., CASE D.A., WRIGHT P.E.; "Three-dimensional solution structure of a single zinc finger DNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUCH
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                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                   PRT; 1350 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multifinger protein Xfin.";
NUCLEIC ACIDS RES. 21:4218-4225(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FINGER PROTEINS. SIMILARITY: CONTAINS 1 KRAB BOX.
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STRUCTURE BY NMR OF FINGER 31.
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SCIENCE 245:635-637(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 6:3065-3070(1987).
STANDARD;
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(REL. 08, I
(REL. 37, I
                                                                                                                                                                 435 DCPFECNQCG 444
                                                                                                                               475 RDPFECNMCG 484
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MEDLINE; 88082679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                         405 -TKEKP----
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01-AUG-1988 (
15-DEC-1998 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 AEESEMPYSYAREYSDYESIKLERHVPYDNSRPTSGKMNCDVCGLSCISFNVLMVHKRSH 139
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Similarity 24.0%; Pred. No. 2.8e-14;
21; Conservative 63; Mismatches 201; Indels 120;
                                                                                              PIR; SO0647; SO0647.

PDB; 12NF: 15-OCT-91.

PROSITE; PSO0028; ZINC_FINGER_C2H2; 35.

PFAM; PPO0096; ZI-C2H2; 36.

ZINC-FINGER; METAL-BINDING; RNA-BINDING; REPEAT; 3D-STRUCTURE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1052 1052
1056 1065
1066 1066
1350 Aa; 155804 MW; 10CA7C8C CRC32;
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KRAB BOX ("B I
ZINC-FINGERS
send an email to license@isb-sib.ch)
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C2H2-TYPE.
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C2H2-TYPE.
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                                                          EMBL; X06021; G65234;
PIR; S00647; S00647.
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us-09-019-348-2.rsp

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and sequencing of a zinc finger cDNA expressed in
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                                                                                                                                                                                                                                                                                                                                                      tch 12.6%;
al Similarity 23.3%;
114; Conservative 5
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                                                                                                                                                                                    SSVYPIALTRADMPMGAPQEMEKKRILL--PEKILPSERGLSPNNSAQDSTDTDSNHEDR 395
                                                                                                                                                                                                                                                                                 447
                                                                                                                                                                                                                                                                                                                  AGVGASGLIYLINHIT-SGVRNGVLPLVKEEQQRQYEAMRASIEIASEGFKVLSGEGEDV 465
                                                                                                             KDEYSDRDENIMKPEPMGDAEESEMPYSYAREYSDYESIKL-----ERHVPYDNS-- 111
                                                                                                                                             111 -RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTG 169
                                                                Gaps
                                                                              1 MEDIQPTVELKSTEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKV 60
                                                                                       PDLGDAASV------EARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRH-
                                                                                                                                                                                                                  396 QH-----LYQQSHVVLPQARNG-MPLLK-EVPRSFELLKPPPICLRDSIKVINKEGEVM
                                                                                                                                                                                                                                                                                                                                              DVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR 503
                                                               50;
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01-AUG-1992 (REL. 23, LAST SECUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BURKE P.S., WOLGEMUTH D.J.; "Zfp-37, a new murine zinc finger encoding gene, is expressed developmentally regulated pattern in the male germ line."; NUCLEIC ACIDS RES. 20:2827-2834(1992).
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MUS.
                                                                Indels
                                                Length
                IK-8)
MISSING (IN IK-4).
MISSING (IN IK-3).
MISSING (IN IK-6 AND F39835EE CRC32;
                                               Score 1211; DB 1; Pred. No. 2.5e-76; Hismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 177-553 FROM N.A.
TISSUB-TESTIES,
MEDLINE: 90301500.
NELKI D., DUDLEY K., CUNNINGHAM P., AKHAVAN M.;
                                                                                                                                                                                                                                                                                                                                                                                             553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                               84;
                        MW;
                                               h 44.4%;
Similarity 48.5%;
50; Conservative 84
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 246
291
291
                       522 AA;
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MEDLINE; 92310982.
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Best Local Simi
Matches 260;
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P17141;
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SEQUENCE
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ZF37_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKPEPMGDAEE----SEMPYSYAREYSDYESIKLERHVPYDNSRPTSGK-MNCDVCGLSC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEH------KERCRAFLQNPDLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCFDANYNPGYMYEKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-BINDING; NUCLEAR PROTEIN; REPEAT;
mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 344; DB 1; Length 553;
Pred. No. 1.1e-16;
55; Mismatches 129; Indels 192;
                                                                              SPERMIOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P -> T (IN REF. 2)
V -> K (IN REF. 2)
F -> V (IN REF. 2)
BB3DF19C CRC32;
                                           NUCLEIC ACIDS RES. 18:3655-3655(1990).
-!- FUNCTION: MAY HAVE A ROLE IN REGULATING
-!- SIMILARITY: CONTAINS 1 KRAB BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN; SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                             EMBL; X64413; G55475; -.
EMBL; X52533; G53457; ALT_INIT.
PIR; S10245; S10245.
PIR; S22954; S22954.
MGD; MGI:99181; ZFP37.
PROSITE: PS00028; ZINC_FINGER_C2H2; 11.
PFM; PPC0096; zf-C2H2; 12.
HSSP; P08047; ISP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
V -> L (IN R
P -> T (IN R
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16;

us-09-019-348-2.rsp

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DATKAPKGSLKDIYKVFNGEGEQIRAFKCEHCRVLFLDHVMYTIHMGCHGYRDPLECNIC 504
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00096; Zf-C2H2; 5.
                                                                                                                                                                                                                                                                                                                                                             STRAIN-SHASTA; TISSUE-THYMOCYTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U92201; G2062742; -.
EMBL; U92200; G2062740; -.
EMBL; U92198; G2062736; -.
EMBL; U92199; G2062738; -.
EMBL; P20199; G2062738; -.
PROSTIE; PS00028; ZINC_FINGER
                                                    505 GYRSQDRYEFSSHIVRGEH 523
                                                                                                                                                                                                                             PROTEIN IKAROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                                                            SALMONIDAE; ONCORHYNCHUS.
                                    GYRSHDRYEFSSHIARGEH
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175
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232
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SEQUENCE FROM N.A.
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HANSEN J.D., STRA
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                                                                                                                                                                                                                               DNA-BINDING
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HAHM K., COBB B.S., MCCARTY A.S., BROWN K.E., KLUG C.A., LEE R., AKASHI K., WEISSMAN I.L., FISHER A.G., SMALE S.T.;
"Helios, a Teall-restricted Ikaros family member that quantitatively associates with Ikaros at centromeric heterochromatin.";
GENES DEV. 12:782-796(1998).
-!- FUNCTION: ASSOCIATES WITH IKAROS AT CENTROMERIC HETEROCHROMATIN.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: RESTRICTED TO THE T-CELL LINEAGE. ABUNDANT IN THYMUS, LOW EXPRESSION IN BONE MARROW AND BRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO DETECTABLE EXPRESSION IN SPLEEN, LIVER, KIDNEY OR MUSCLE.
ALTERNATIVE PRODUCTS: TWO FORMS OF THIS PROTEIN; HELIOS A AND
B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE IKAROS FAMILY OF ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||| ||:| |: :|: |||| |
|GAEALHPLMQHAPSTIAEVAPVISSAYSQVYHPNRIERPISRETSD---SHENNMDGPTS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 ELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDYESIKLERHVPYDNSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGAS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLEEHKERCRAFLQNPDLGDAASVEARHIK-------AEMGSERALVLDR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSLEEHKERCHNYLQNVSMEAAGQVMSHHVPPMEDCKEQEPIMDNNISLVPFERPAVIEK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LASNVAKRKSSMPQKFIGEKRHCF---DANYNPGYMYEKENEMMQTRMMDQAINNAISYL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLPEKILPSERGLSPNNSAQDSTDTDSNHEDRQHLYQQSHVVLPQARNGMPLLKEVPRSF 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHEIENVDSREAPANEDEDAGEDSMKVKDEYSDRDENIMKPEPMGDAEESEMPYSYAREY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSHMISINSVKLEMOSDEECDRQPLSREDEIRGHDEGSSLEEPL--IESSEVADN--RKV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAEAFRPLVQTPPAPTSEMVPVISSVY-----PIALTRADMPMGAPQEMEKKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P08047; 1SP2. _ TRANSCRIPTION REGULATION; ACTIVATOR; ZINC-FINGER; METAL-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.2%; Score 1234; DB 1; Length 526;
49.7%; Pred. No. 6.7e-78;
tive 67; Mismatches 138; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN HELIOS A).
AD142BD4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                      R PROTEIN; ALTERNATIVE SPLICING.
2119 ZINC-FINGERS I.
523 ZINC-FINGERS II.
134 C2H2-TYPE.
                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 248;
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SEQUENCE
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ZN_FING
ZN_FING
ZN_FING
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ZN_FING
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                                                                                                                                                                                                                                                                                                                                      ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amphibian species."

EUR. J. IMMUNOL. 27:3049-3058(1997).

EUR. J. IMMUNOL. 27:3049-3058(1997).

I FUNCTION: BINDS AND ACTIVATES THE ENHANCER (DELTA-A ELEMENT) OF THE CD3-DELTA GENE. FUNCTIONS IN THE SPECIFICATION AND THE MATURATION OF THE T LYMPHOCYTE. ALSO INTERACTS WITH A CRITICAL CONTROL ELEMENT IN THE TPO (TEMNINAL DEOXYNOLEDOTIDYLTRANSFERASE) PROMOTER AS WELL AS WITH THE PROMOTERS FOR OTHER GENES EXPRESSED DURING EARLY STAGES OF B AND T CELL DEVELOPMENT.

-: SOBGELLULAR LOCATION: NUCLEAR.

-: SUBSELLULAR LOCATION: NUCLEAR.

-: STGHT FORMS OF THE PROTEIN; IKL-IKB; ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE IS THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HANSEN J.D., STRASSBURGER P., DU PASQUIER L.; "Conservation of a master hematopoietic switch gene during vertebrate evolution: isolation and characterization of Ikaros from teleost and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: EXPRESSION BEGINS AT DAY 3-4 IN THE YOLK SAC AND AT DAY 5-6 IN THE EMBRYO PROPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE IKAROS FAMILY OF ZINC-FINGER PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: EXPRESSION MAINLY LIMITED TO THYMUS, SPLEEN, AND PRONEPHROS. VERY LOW EXPRESSION IN LIVER. NO EXPRESSION IN TESTIS, BRAIN, EYE AND MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVATOR; ZINC-FINGER; METAL-BINDING;
EIN; ALTERNATIVE SPLICING.
ZINC-FINGERS II.
ZINC-FINGERS II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IK-2, IK-4 AND IK-8).
IK-6).
IK-5).
TYRALONCMY STANDARD; PRT; 522 AA. 013089; 013088; 013086; 013087; 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
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MEDLINE: 95021239.

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DIDSNHEDRQHLYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEV 446
                                                                                                              447 MDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR 503
                                                                                                                                                                                                                    IKAR_MOUSE STANDARD; PRT; 517 AA.

003267; 064044; 064051;
01-OCT-1993 (REL. 27, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DNA-BINDING PROTEIN IRAROS (LYMPHOID TRANSCRIPTION FACTOR LYF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC, T01470;
TRANSCRIPTION REGULATION; ACTIVATOR; ZINC-FINGER; METAL-BINDING; DINA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING.
DOMAIN
117 223
ZINC-FINGERS I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALLA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEORGOPOULOS K., MOORE D.D., DERFLER B.;
"IKAROS, an early lymphoid specific transcription factor and
putative mediator for T cell commitment.";
SCIENCE 258:808-812(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:96535; IKAROS.
PROSITE; PS00028; ZINC_FINGER_C2H2; 4.
PFAM; PF00096; zf-C2H2; 4.
iiSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1)
SEQUENCE FROM N.A. (ISOFORM 5).
TISSUE-EMBRYO;
MEDLINE: 93068267.
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EMBL: S74517; G807149; ALT_SEQ.
EMBL: S74518; G807151; -
EMBL: S74708; G807153; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKAROS OR LYF1.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                RESULT 3
IKAR_MOUSE
                                                                                                                                     399
                                                                            387
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17;
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M -> VAYGADGFRDFHAIISDRGM (IN ISOFORMS II AND IV).

MISSING (IN ISOFORM V).

MISSING (IN ISOFORMS I AND II).

MISSING (IN ISOFORMS III AND IV).

VC -> MY (IN REF. 2).

VC -> MY (IN REF. 2).

WISSING (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---MGAPQEMEKKRILLPEKILPSERGLSPNNSAQDSTDTDSNHEDRQH--LYQQSHVVL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 RACEMNGEECAEDLRMLDASGEKMNGSHRDQGSSALS-----GVGGIRLPNGKLKCDI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEYSDRDENI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSNHSAQDAVDNLLLLSKAKSVSSEREASPSNSCQDSTDTESNAEEQRSGLIYLTNH-IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 MKPEPMG------DAEESEMPYSYAREYSDYESIKLERHVPYDNSRPTSGKMNCDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVYPIALTRADMP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHARNGL-ALKEEQRAYEVLRAASENSQDAFRVVSTSGEQLKVYKCEHCRVLFLDHVMYT
                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                  Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELIOS.
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.9%; Score 1279.5; DB 1; Length Best Local Similarity 52.7%; Pred. No. 4.8e-81; Matches 274; Conservative 71; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 246-267 AND 289-306.
STRAIN-BALB/C; TISSUE-THYMUS;
MEDLINE; 98180981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHM---GCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
210C FINGER PROTEIN HELLOS.
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    ZINC-FINGERS
                          C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
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                                                                                                                                                                                      140
282
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235
482
  479
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1194
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54
141
234
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517 AA;
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P81183;
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CONFLICT
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                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                   STEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEYSDRDENI 71
                                                                                                                                                                                                                                                                  | :| | :::|| | :| | :| | :| | SGKESPPVSDIPDE-GDEPMPIPEDLSTISGGQQSSKSDRVVASN---VKVETQSDEENG
                                                                                                                                                                                                                                                                                                                                                                 HVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 -EARHIK-----AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCFDANYNPGYMYE
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                                                                                                                                                                                                                             47;
                                                                                                                                                                                                  49.1%; Score 1339.5; DB 1; Length 519; 53.6%; Pred. No. 3.6e-85;
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GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVE
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                           71; Mismatches 124; Indels
MISSING (IN IK4).
MISSING (IN IK2).
MISSING (IN IK6).
MISSING (IN IK6).
MISSING (IN IK5).
OV -> FS (IN REF. 2).
S -> T (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
S -> T (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
KPLA -> RRS (IN REF. 2).
WHA -> RRS (IN REF. 2).
                                                                                                                                                  ARNGL -> RRAQRV (IN REF. 5A97272D CRC32;
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DNA-BINDING PROTEIN IRAROS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518 AA
                                                                                                                                                    PHARNGL
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STRAIN-H.B2; TISSUE-THYMUS;
MEDLINE; 97439462.
                                                                                                                                                               57528
                                                                                                                                                                                                              Local Similarity 53.6 tes 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                AA;
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042410;
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: EXPRESSED EARLY IN EMBRYO FROM EMBRYONIC DAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAF 226
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                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE IKAROS FAMILY OF ZINC-FINGER PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQNPDLG------DAASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 DEAQDMSQVSGKESPPISDVPDDA--DEPMPVPEDLSTTTGGQQSVKNERVLAG----NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00028; ZINC_FINGER_C2H2; 5.
PFAM; PF00096; Zf-C2H2; 5.
TRANSCRIPTION REGULATION; ACTIVATOR; ZINC-FINGER; METAL-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 1; Length 518; 3e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN; ALTERNATIVE SPLICING
24 ZINC-FINGERS I.
21 ZINC-FINGERS II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1321.5; DB 1;
; Pred. No. 6.3e-84;
66; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC32;
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C2H2-TYPE.
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52.0%;
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57586 N
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Best Local Similarity 52.0%
Matches 279; Conservative
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518 AA;
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SEQUENCE
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Compugen Ltd.
GenCore version
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sw model using protein search, 21 protein

(without alignments) 1057.714 Million cell updates/sec November 6, 1999, 09:57:36 ; Search time 13.55 Seconds Run on:

US-09-019-348-2 2728 score:

1 MEDIQPTVELKSTEEQPLPT......HDRYEFSSHIARGEHRAMLK Title: Perfect sc Sequence:

BLOSUM62 Scoring table:

SwissProt_37:* **Database**

77977 seqs, 28268293 residues Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	Description	13422 homo sapie	42410 gallus	57 mus mus	81183 mus mus	13089 oncorhy	17141 mus muscu	08045 xenopus la	01791 trib	61967 mus	15620 mus muscu	06730 homo	18723 xenopus l	18714 xenopus l	17098 homo sapi	18747 xenopus 1	03923 homo sapi	203	62981 rattus no	28160 homo	03309 mus	07230 mus	28698 home	13360 hom	05481 homo	08043	62513 mus	06732 home	99676 hото	75820 homo	13682 homo	28151 bos t	15072 homo	51523 homo	61751 mus n	14628 homo	10076 mus n	51786 homo sa	15928 homo sapi	18744 xenopus	02386 homo'sa	60821 mus muscu	51814 homo sa	52742 homo sapi
SUMMARIES	di .	IKAR_HUMAN	IKAR_CHICK	IKAR_MOUSE	HELI MOUSE	I KAR_ONCMY	ZF37_MOUSE	XFIN_XENLA	HUNB_TRICA	ZF90_MOUSE	ZF35_MOUSE		ZG48_XENLA	ZG20_XENLA	ZN08_HUMAN	ZO28_XENLA	ZN85_HUMAN		OZF_RAT	ZN43_HUMAN	MLZ4_MOUSE	ZF29_MOUSE	ZN42_HUMAN	2177_HUMAN	ZN91_HUMAN	KR2_MOUSE	OZF_MOUSE	Z11B_HUMAN	. 2184_HUMAN	Z189_HUMAN	ZN35_HUMAN	OZF_BOVIN	OZF_HUMAN	8 8	100	136	F26	Z157_HUMAN	141	ZO20_XENLA	ZN45_HUMAN		N4.	135_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLINER A., WU P., LARGESPADA D.A., VORTKAMP A., SCHERER S.,
MOLINER A., WU P., LARGESPADA D.A., VORTKAMP A., SCHERER S.,
COPELAND N.G., JENKINS N.A., BRUNS G., GEORGOPOULOS K.;
The Ikaros gene encodes a family of lymphocyte-restricted zinc
if inger DNA binding proteins, highly conserved in human and mouse.";
J. IRMUNOL. 156:585-592(1996).

- I- FUNCTION: BINDS AND ACTIVATES THE ENHANCER (DELTA-A ELEMENT) OF
THE CO3-DELICAT GENE. FUNCTIONS IN THE SPECIFICATION AND THE
MATURATION OF THE LYMPHOCYTE. ALSO INTERACTS WITH A CRITICAL
CONTROL ELEMENT IN THE TOT (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE)
PROMOTER AS WELL AS WITH THE PROMOTERS FOR OTHER GENES EXPRESSED
OURING EARLY STAGES OF B AND T CELL DEVELOPMENT.

- I- SUBCELLULAR LOCATION: NUCLEAR.

- I- SUBCELLULAR LOCATION: NUCLEAR.

- I- SUBCELLULAR LOCATION: NUCLEAR.

- I- SUBCELLULAR LOCATION SMALL INTESTINE.

- I- SUBCRELULAR SMALL INTESTINE.

- I- ALTERNATIVE PRODUCTS: SIX FORMS OF THE PROTEIN; ISOFORMS IXI-IK6;

- ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE IS
P51522 homo sapien
P21506 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE IKAROS FAMILY OF ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE: 96252222.
NIETFELD W., MEYERHANS A.;
"Cloning and sequencing of hik-1, a cDNA encoding a human homologue
                                                                                                                                                                                                                                                                    IKAR_HUMAN STANDARD; PRT; 519 AA.
13.422; 000598;
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DNA-BINDING PROTEIN IKAST ANNOPATION UPDATE)
IKAROS OF IKI OR OR LYFI.
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PROTEIR; ALTERNATIVE SPLICING.
24 ZINC-FINGERS I.
ZINC-FINGERS II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
TISSUE-BONE MARROW;
                                                                                                                        ALIGNMENTS
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C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
   ZN83_HUMAN
ZN10_HUMAN
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MIM; 603023; -.
PROSITE; PS00028; ZINC_FINGER_C2H2; 5.
PFAM; PF00096; ZE-C2H2; 5.
TRANSCRIPTION REGULATION; ACTIVATOR; Z.
DNA-BINDING; NUCLEAR PROTEIN; ALTERNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOL. LETT. 49:139-141(1996).
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   428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMAN)
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ZN_FING
ZN_FING
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IKAR_HUMAN
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us-09-019-348-2.rpr

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C.Accession: 828823
K.Lovering, R.; Trowsdale, J.
Nucleic Acids Res. 19, 2921-2928, 1991
A.Title: A gene encoding 22 highly related zinc fingers is expressed in lymphoid cell li
A.Reference number: $26823; MUID:91279444
A.Reference number: $26823; MUID:91279444
A.Reference number: $26823
A.Stetus: preliminary
A.Molecule type: mRNA
A.Residues: 1-803 <LOV>
A.Residues: 1-803 <LOV>
C.Genetics: EMBL:X59244; NID:938031; PID:938032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                          C:Species: Homo sapiens (man)
C:Date: 13-Jan 1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1998
448 -----THMGCHGFRDPF 478
                                          393 STHISPSIEFGVQITEDNHQSPSKDHIGEKPFSCSECGKSFFYKSVLKDHLVVHIGEKPY 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 EESEMPYSYAREYSDYESIKLERHVPYD-----NSRPTSGKM-----NCDVC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYAC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.8%; Score 295.5; DB 2; Length 803; Best Local Similarity 37.3%; Pred. No. 1.1e-13; Matches 59; Conservative 29; Mismatches 51; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 QRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHK 220
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Job time: 71 sec
                                                                                                                          453 HCIECGRSYTHQSSLKSHQR 472
                                                                                          479 ECNMCG-----YRSHDR 490
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A.Map position: 19p13.1-19p12
C.Keywords: DNA binding
                                                                                                                                                                                                                                                                    finger protein ZNF43 - human
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A:Cross-references: GDB:132279 A:Map position: 19p12-19p12	Db 363 KIRHKCPDCPKTFKTPGTLAMHRKIHTGEADATPKERPYT
Query Match 10.9%; Score 297.5; DB 2; Length 595; Best Local Similarity 24.0%; Pred. No. 5.4e-14; Matches 103; Conservative 63; Mismatches 148; Indels 115; Gaps 19;	
	DD 453 GEKPFHCGICERSFSVRDILIRHIRTRIGERPYTCPYCDKRFTQRSALIVH 503 RESULT 14
2; 179 NYACQRRDALIGHLRTHSVEKPYKCEFCGRSY 210	S51037 Zinc-finger protein - African clawed frog C:Species: Xenopus laevis (African clawed frog)
Qy 211 KQRSSLEEHKERC-RAFLQNPDLGDAASVEARHIKAEMGSERALVLDRL 258	
27 259 ASNVAKRKSSMPQKFIGEKRH-CFDANNNPGYMYEKENEMMQTRMMDQAINNAISYLG 315	A;Title: Sequence-specific recognition of a repetitive DNA element by a C(2)H(2) zinc A;Reference number: S51037 A;Accession: S51037 A;Accession: S51037 A;Status: preliminary
OY 316 AEAFRPLVQTPPAPTSEMVPVISSVYPIALTRADMPMGAPQEMEKKRILLPEKILPSER- 375 Db 423 EKPYKSKECEKAFNQSSKLTEHRKIHTGEKPYECEKC 459	A;Molecule type: DNA A;Residues: 1-675 <sch> R:Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Kno J. Mol. Biol. 208, 639-659, 1989</sch>
QY 375 GLSPNNSAQDSTDTDSNHEDRQHLYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLR 434 : : : : : : Db 460 GKAFNQSSNLTRHKKSHTEEKPY	A;Title: Second-order repeats in Xenopus laevis finger proteins. A;Reference number: 805632; MUID: 90040698 A;Accession: 805565 A;Status: not compared with conceptual translation
LDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFS 494	A;Molecule type: mRNA A;Residues: 85-448,/K',450-613 <nie> A;Experimental source: clone XlcGF20-1 C;Keywords: DNA binding; zinc finger</nie>
	Query Match Duery Match Duery Match Duery Match Duery Matches 119; Conservative 87; Mismatches 179; Indels 175; Gaps 24;
RESULT 13 A36901 Chorion transcription factor CF2-I (alternatively spliced) - fruit fly (Drosophila melan	QY 14 EEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEY 64
C.Dater. 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997 C.Accession: A36901 R.Hau, T.; Gogos, J.A.; Kirsh, S.A.; Kafatos, F.C. Science 257, 1946-1960, 1992	OY 65 SDRDENIMKPEPMGDAEESEMPYSYAREYSDYESIKLERHV-PYDNSRPTSGKMNCDVCG 123 :
A; Title: Multiple zinc finger forms resulting from developmentally regulated alternative A; Reference number: A36901; MUID:93030711 A; Accession: A36901	OY 124 LSCISFNVLMVHRRSHTGERPFOCNOCGASFTOKGNLLRHIKLHTGEKPFKCHLCNYACQ 183 1
A:Molecule type: DNA A:Rolecule type: DNA A:Residues: 1-510 <hsu> A:Note: sequence inconsistent with nucleotide translation A:Note: sequence avtracted from NPT hawken (MPDTN:114070 MPDTN:114000</hsu>	QY 184 RRDALTGHLRTHSVEKPYKCEFGGRSYKQRSSLEEHKERCRAFLQNPDLGDAASVEARHI 243 :
07.	OY 244 KAEMGSERALVLDRLASNVAKRKSSMPOKFIGEKRHC 280
Query Match 10.9%; Score 296.5; DB 2; Length 510;	OY 281 FDANYNPGYMYEKENEWMOTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVI 337 :
best Loc Matches	
QY 6 PTVELKSTEEQPLP-TESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSM 59 : : : : : : : Db 309 PQVIIKEEPLSLSDSGDVVNSVP-VYAIQANPGVPAPASSGVLVGTQTVPADLAH 362	LPSTESGGTFSNEHELLTHQSTHTE FELLKPPPICLRDSIKVINKEGEVM
OY 59 KVKDEYSDRDENIMKPEPMGDAEESEMPYSYAREYSDYESIKLERHVPYD 108	

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505556
finger protein (clone XlCOF28) - African clawed frog (fragment)
(Specias: Xenopus laevis (African clawed frog)
(Spate: 28-Reb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-1993
C.Date: 28-Reb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-1993
A.Date: 28-Reb-1990 #sequence_revision A.Dec-1993
A.Reference number: 805632; MUID:90040698
A.Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-439 <NIE>
C.Keywords: DNA binding: 21nc finger
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CiSpecies: Homo sapiens (man)
CiSpecies: Local-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
CiSpecies: Of 202075
Riphocelet, D.A.
Submitted to the EMBL Data Library, September 1995
A;Reference number: G09169
A;Accession: G02075
A;Accession: G02075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-595 <PON>
A;Residues: 1-595 <PON>
CiSpecies: CiSpecies: EMBL:U35376; NID:g1017721; PID:g1017722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEEHKERCRAFLQNPDLGDAASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- XTHESKPQQ--- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 EKRHCFDANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 EL----PEAINSVESP-EAIDDYEKNYI--PWSPLSEYLGVFLPPEKQHKCTECDKCFLE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROHL -- YQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVIN--KEGEVMD-- 449
245 RIHTGERPYMCKECGKAFSQNSSLVQHERIHTGDKPYKCAECGKSFCHSTHLTVHRRIHT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VISSVYPIALTRADMPMGAPQEMEKKRILLPEKILPSERGL-SPNNSAQDSTDTDSNHED 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Mismatches 136; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.9%; Score 298; DB 2; 24.7%; Pred. No. 3.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449 -VFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCG 484
                                                                                                       305 GEKPYECQDCGRAFNQNSSLGRHK 328
                                                197 VEKPYKCEFCGRSYKORSSLEEHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98; Conservative
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Best Local S
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C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 14-Aug-1998
C:Accession: B34612
R:Lania, L.; Donti, E.; Pannuti, A.; Pascucci, A.; Pengue, G.; Feliciello, I.; La Mantia Genomics 6, 333-340, 1990
A:Title: CDNA isolation, expression analysis, and chromosomal localization of two human A:Reference number: A34612; MUID:90169993
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                                                                                                                           KCEFCGRSYKQRSSLEEHKE-----RC-RAFLQNPDLGDAASVEARHIKAEMGS 249
                                                                                                                                                                                                                                                                                                        K-----PYKCSECGKAFNQSSVLILHQRIHTGEKPY-PCNQCTKS----FSRLSD-LINH 346
                                                                                                                                                                                                                                                                                                                                                                                                                                391 KTFSQSSNLILHQRIHTGEKPYPCNSCSKSFSRGSDLIKHQRVHTGEKPYTCNLCSKSFS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 TDTDSNHEDRQH------LYQQSHVVL------PQARNGMPLLKEVPRS 422
                                                                                                                                                                                                                                                              ERALVLDRLASNVAKRKSSMPQKFIGEKRHCFDANYNPGYMYEKENEMMQTRMMDQAINN 309
                                                                                                                                                                                                                                                                                                                                                                                          310 AISYLGAEAFRPLVQTPPAPTSEMVPVISSVYPIALTRADMPM-----GAPQEMEK-- 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRKEEGLPEEEPSHVTGREGFPTDAPYPTTLGKDRECQSQSLALKEQNNLKQLEFGLKEA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: | :| | :| | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-543 < LAN>
A; Cross-references: GB:M29581; NID:g340447; PID:g340448; GB:J04751
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 543;
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Best Local Similarity 29.9%; Pred. No. 4.1e-14;
Matches 79; Conservative 40; Mismatches 80
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A;Map position: 20q13-20q13
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zinc finger protein ZNF8 - human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 PCAQCGKSFSQRSDLVNH 569
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224 RAFLQNPDLGDAASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCFDA : : 170DSAN	405 -TKEKP
Qy 284 nynpgymyekenemmotrmmdoainnaisylgaeafrplvqyppaptsemypvisssypi 343 : : : :	35
Qy 344 ALTRADMPMGAPQEMEKKRILLPEKILPSERGLSPNNSAQDSTDTDSNHEDRQH 398 1	
OY 398 LYQOSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHV 457 1	10-sep-19
Qy 458 LFLDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR 503 : : : :	A;Title: Cloning and sequencing of a zinc finger cDNA expressed in mouse testis. A;Reference number: S10245; MUID:90301500 A;Accession: S10245 A;Molecule type: mRNA A;Residues: 1-411 <nel></nel>
t d	A;Cross-references: EMBL:X52533; NID:q53456; PID:q53457 C;Keywords: DNA binding; zinc finger
Inger procein zip-3/ - mouse C.Species: Mus musculus (house mouse) C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 13-Sep-1998 C.Accession: S22954	Query Match 11.7%; Score 319; DB 2; Length 411; Best Local Similarity 24.6%; Pred. No. 9.8e-16; Matches 95; Conservative 41; Mismatches 88; Indels 162; Gaps 12;
R:Burke, P.S.; Wolgemuth, D.J. Nucleic Acids Res. 20, 2827-2334, 1992 A;Title: 2fp-37, a new murine zinc finger encoding gene, is expressed in a developmental	K-MNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 170
A;ACC6SION: S.ZZ#54 A;Molecule type: mRNA A;Residues: 1-553 <bur> A;Cross-references: EMBL:X64413; NID:g55474; PID:g55475</bur>	Qy 171 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEH 220
	QY 220 -KERCRAFLQNPDLGDAASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIGEKR 278
Query Match Best Local Similarity 23.3%; Pred. No. 2.3e-17; Matches 114; Conservative 55; Mismatches 129; Indels 192; Gaps 16;	279 HCFDANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVIS
OY 21 ESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEXSDRDENI 71	339
CY 72 MKPEPMGDAEESEMPYSYAREYSDYESIKLERHVPYDNSRPTSGK-MNCDVCGLSC 126	Db 223YGSSLTKHMRIHTGEKPFECNECGKTF 249 QY 399 YQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVL 458
127 ISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGERPFKCHLCNYACQRRD	484
187	Db 277 FGHSSSLTYHMRTHIGDCPFECNQCG 302
284 ALTDHLRIHTGEKPYKCNECGKTFRHSSNLMQHLRSHTGEKPYECKECGKSFRYNSSL 235 AASVEARHIKAEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCFDANYNPGYMYEKE 1	
	C;Date: 30-Sep-1949 #sequence_revision 30-Sep-1989 #text_change 31-Dec-1993 C;Accession: 800647 R;Ruiz 1 Altaba, A.; Perry-O'Keefe, H.; Melton, D.A. EMBO 1. 6, 3065-3070, 1987
Db 360 372 Ov 355 POEMEKKRIILPEKII.PSERGISPUNSAODSTDTDSNHEDBOHLYGOSHVVI.DOABNGMP 414	A;Title: Xfin: an embryonic gene encoding a multifingered protein in Xenopus. A:Reference number: S00647; MUID:88082679 A:Arceston: end647
372HMRIHTGEKPFECNECGKTFSKKSHLVİHQKTH	A: MOLECULE LYPE: MRNA A: MOLECULE LYPE: MRNA A: MOLECULE LYPE: MRNA A: ACREGICES: 1-1350 < RUE: ACREGICES: ACREGICES: 1-1350 < RUE: ACREGICES: ACREGI
QY 415 LLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHMGCHGF 474	A;NOTE: it is uncertain whether Met-1, Met-11, Met-16, Met-38, or Met-39 is the initi C;Genetics:

223

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lymphoid transcription factor Ikaros/LyF-1, form IV - mouse
NyAlternate names: Ikaros/LyF-1 form I; Ikaros/LyF-1 form II; Ikaros/LyF-1 form III
NyAlternate names: Ikaros/LyF-1 form I; Ikaros/LyF-1 form III; Ikaros/LyF-1 form III
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
C;Accession: A56229
R;Hahm, K.; Ernst, P.; Lo, K.; Kim, G.S.; Turck, C.; Smale, S.T.
R;Hahm, K.; Ernst, P.; Lo, K.; Kim, G.S.; Turck, C.; Smale, S.T.
A;Title: The lymphoid transcription factor LyF-1 is encoded by specific, alternativel
A;Reference number: A56229; MuID:95021239
A;Accession: A56229; MuID:95021239
A;Accession: A56229; MuID:95021239
A;Accession: A56229; MuID:95021239
A;Accession: A56229

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                                  48 NEDED----AGEDSMKVKDEYSDRDENIMKPEPMGDAEESEMPYSYAREYSDYESIKLER 103
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                                                                                                                                                                                       | :| | :::|| | :| | :| | SGKESPPVSDTRGAQQNSKSDRGMVAYGADGFRDFHAIISDR
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                                                                                                                                                        HVPYDNSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRH
                                                                                                                                                                                                                                                                             IKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERC
                                                                        449 VFRCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR 503
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C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
C;Accession: B56229
C;Accession: B56229
A;Tibahn, K.; Ernst, P.; Lo, K.; Kim, G.S.; Turck, C.; Smale, S.T.
Mol. Cell. Biol. 14, 7111-7123, 1994
A;Title: The lymphoid transcription factor LyF-1 is encoded by specific, alternatively A;Reference number: A56229; MUID: 95021239
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-427 cHAM>
A;Residues: 1-427 cHAM>
A;Cross-references: GB:S74518
C;Keywords: alternative colline
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#sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
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R; Georgopoulos, K.; Moore, D.D.; Derfler, B.
R; Georgopoulos, K.; Moore, D.D.; Derfler, B.
S; Georgopoulos, R.; Moore, D.D.; Derfler, B.
S; Georgopoulos, R.; Mos 812, 1992
A; Title: Ikaros, an early 1ymphoid-specific transcription factor and a particle: Ikaros, an early 1ymphoid-specific transcription factor and a particle. Ikaros, and Early 159572
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
42.4%; Score 1156; DB 2;
Best Local Similarity 51.3%; Pred. No. 9.2e-76;
Matches 245; Conservative 64; Mismatches 93;
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Best Local Similarity 50.98
Matches 242; Conservative
02-Aug-1996
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h.closs-leferent
C.Genetics:
A.Gene: Ikaros
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

November 6, 1999, 08:07:40 ; Search time 18:18 Seconds (without alignments) 1117.338 Million cell updates/sec Run on:

US-09-019-348-2 2728 1 MEDIQPTVELKSTEEQPLPT......HDRYEFSSHIARGEHRAMLK 507 .Tille: Perfect score: Sequence:

BLOSUM62 Scoring table: 122810 segs, 40065486 residues Searched:

Database :

PIR_60:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPTEC

		Description	A-binding prote	DNA bindin	ymphoid trar	d transcri	inger protein zf	inger protein, t	,	gene NK10 protein	ş.	zinc finger protei	<u>د</u>	iption	U	inc-finger p	inger protein	finger	inger protein	er prote	inc finger	ч	finger	ment	er prote	ΗF	scription a				protei	inger protein	r protein	opel-relate	inger pro	protein	finger protein HZF	el-type z	inger prote	inger protein 1	finger pro
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467 IHM---GCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR 503

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1 276.5 10.1 276 20000010 21.1 21.1 21.1 21.1 21.1 21.1 2	finger protein kox finger protein (cl finger protein XFO zinc finger protei Z13 protein - mous renal transcriptio		-1995 #text_change 19-Oct-1995 functionally diverse zinc finger DNA-bin eptual translation	DB 2; Length 518; 5e-85; ss 129; Indels 46; Gaps 17;	NEDEDAGEDSMKVKDEYSDRDENI 71 	DAEESEMPYSYAREYSDYESIKLERHVPYDNSRPTSGKMNCDV 121 : - - - - - - - - - - -	SNLARHIKLHTGEKPFKCHLCNYA 181 	SHKERCRAFLONPDLGDAASV 238 : : : SHKERCHNYLESMGLPGMYPVIKE 241	OKFIGEKRHCF-DANYNPGYMYE 292 : : QKFLGDKCLSDMPYDSA-NYE 298	TSEMVPVISSVYPIALTRADMP- 352 	QDSTDTDSNHEDRQHLYQQSHVVL 406 	SCEVMDVFRCDHCHVLFLDYVMFT 466 : : : : : SCEQLKVYKCEHCRVLFLDHVMYT 474
## 10 276.5 10.1 462 2 42 42 276 10.1 453 2 43 2 44 276 10.1 348 2 44 276 10.1 348 2 44 276 10.1 348 2 276 10.1 348 2 275 10.1 348 2 275 10.1 348 2 275 10.1 348 2 275 10.1 348 2 275 10.1 348 2 2 275 10.1 348 2 2 275 10.1 348 2 2 2 28303 2.4 2 2.4	\$10397 \$65844 \$65086 138599 A48157	ALIGNMENTS	use 19-Oct 11y of 058 th conc	Score 1286; Pred. No. 5 9; Mismatche	PHEIENVDSREAPAN :: PEDLSTISGAQQN	EMPYSYAREYSDYES : : : KMNGSHRDQGSSALS	PFQCNQCGASFTQKG 	EFCGRSYKQRSSLEE : GYCGRSYKQRSSLEE	DRLASNVAKRKSSMP 	Saeafrplvotppaf : Saeslrplvotppg-	PSERGLSPNNSAQDS 	PPICLRDSIKVINKE : :: :: ASENSQDAFRVVSTS
# 40 276.5 10.1 462 41 276 10.1 353 42 276 10.1 353 43 276 10.1 353 44 276 10.1 353 44 276 10.1 354 45 275 10.1 576 Ma-binding protein lkaros food species: Mus musculus (hous) included to the species of the sp	000000		e m e m des des des des des	# # H H	LPK) :- MPV)	EESI	GERI GERI GERI	YKC: :	LVL!	SYL(:11 NYL(KILI : KSV:	LKPI : LRA
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	444 443 2443		RESULT A56355 DNA-bindi C;Species C;Date: 1 C;Acces: 4 R;Molnar, Mol. Cell A;Referen A;Referen A;Status: A;Referes A;Accessi A	Query N Best Lo Matches	Oy 12 Db 13	Qy 72 Db 69	Oy 122 Db 122	ထ ထ	Qy 239 Db 242	σ	വ	Oy 407 Db 416

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qq	. 393	1: : : : : :
οy	260	260 SNVAKRKSSMPQKFIGEKRHCFDANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAF 319
qq	431	431 SPAASSLSSYPSPV
δý	320	
qq	449	449 -PSPATISFPSPVPISYSSPG-SSTYPSPAHSGFPSPSVATIFASVPPAFPIQVSS 503
οy	365	365 LPEKILPSERGLSPNNSAQDSTDTDS 390
q	503	
Sear	ch com time:	Search completed: November 6, 1999, 09:41:35 Job time: 67 sec

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--FDANYN---PGYMYE 292
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                                                                                                                                                                                                                                                            236 IKVDPMPPFQLGAAPENGLDGGLPPEVHGLVLAAPEEAPQPMPPLEPLEPLEPLEPLEPLEPM 295
                                                                                                                                                                                                                                                                                                                                                       296 ОЅLЕРLQPLEPMQPLEPMQPLEPMQPLEPLEPMQPLEPMQPLEPMQPLEPMQPMQPMTPMQPMQPM 355
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                                                                                                                                                                                                                                                                                                           338 SSVYPIALTRADMPMGAPQEMEKKRILLP----EKILPSE--RGLSPNNSAQDSTDTDSN 391
                                                                                                                                                               177 VHTGCKDFLCQFCAQRF-GRKDHLTRHTKKTHSQELMQENMQAGDYQSNFQLIAPSTSFQ
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PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                   392 HEDRQHLYQQSHVVLPQARNGMPLLKEVPRSFEL-----LKPPPICLRD 435
                                                                                                                                                                                                                                                                                                                                                                                                                                 356 QPWQPMLPWQPWLPWQPWLPMPEPSFTLHPGVVPTSPPIILQE 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO
TITLE OF INVENTION: PUNCTIONAL DOMAINS OF DNA BINDING
NUMBER OF SOUDENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: Arnold, White & Durkee
321 No. 5763209th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/040,548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                           236 ASVEARHIKAEMGSERALVLDRLASNVAKRKSSMP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REGISTRACE/DOCKET NUMBER: arcd067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: Floppy disk
IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
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TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
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                                                                                                                                                                    |: : |: | | | | | | 305 TNRYDHYTAHLKHHTRAGDNER----VYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGK 360
                                                                                                                                                                                                                                                               361 CNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSSQKTHLITHMRTHSGEKPFKCDQCSYV 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 CDVCGLSCISFNVLMVHKRSHTGERPFQCN--QCGASFTQKGNLLRHIKLHTGEKPFKCH 176
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                                                                                                                                                                                                                                                                                                                                                                                                                       VEAR----HIKAEMGS--ERALVLDRL-ASNVAKRKSSMPQKFIGEKRHCFDANYNPGYMY 291
193 SLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFRCKPC-QYEAESE 251
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                                                                                                                                                                                                                                                                                                                                                          ----FNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYA
                                                                                                                                                                                                                                                                                                                            182 CORRDALTGHLR-THSVEKPYKCEFCGRSYKORSSLEEHKE---RCRAFLQNPDLGDAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMGAPQEMEKKRILLPEKILPSERGLSPNNSAQDSTDTDSNH----EDRQHLYQQSHVVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKENEMMQTRMM-DQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVYPIALTRADM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526 ---TELEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPSNNVSVIQVTTRTRKSVTEVKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 KKCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release.#1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,661
                                                                                                                                         REYSDYESIKLERHV-PYDNSRPTSGKMNCDVCGLSCIS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.2%; Score 224.5; DB 2;
21.7%; Pred. No. 6e-14;
tive 52; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OARNGMPLLKEVPR---SFELLKPPPICLRDSIK 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08718661
Patent No. 5876972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 21.7
tes 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nucl
TITLE OF INVENTION: tumo
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 667 amino acids TYPE: amino acid
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; MOLECULE TYPE: protein
US-08-718-661-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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US-08-718-661-2
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231 EQQEGLLSEVNAEKVVGNMKPPKPTKIKKKGVKKTFQCELCSYTCPRRSNLDRHMKSHTD 290
                                                                                                                                                                                       201 YKCEFCGRSYKQRSS-----LEEHKERCRAF-----LQNPDLGDAASVEARHIKAE 246
      407 YECYICHARFTQSGTMKMHILQKHTENVAKFHCPHCDTVIARKSDLG--VHLRKQHSYIE 464
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                                                                                                            291 ERP----HKCHLCGRAFRTVTLLRNHLNTHTGTRPHKCPDCDMAFVTSGELVRHRRYKHT
                                                                                 110 SRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLL-----
                                                                                                                                                              162 --------RHIKLHIGEKPFKCHLCNYACQRRDALIGHLRIHSVEKP
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Pred. No. 3.5e-15;
1; Mismatches 203; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40, Application US/08398590A
Patent No. 5935811
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Schoenherr, Christopher J.
TITLE OF INVENTION: Neuron-Restrictive Silencer Factor
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,590A
FILING DATE: 03-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A-60897/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 237; 22.4%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,445
FILING DATE: 06-AUG-1995
ATTORNEY/AGENT INFORMATION:
RAME: S11va, RObin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
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TELERAX: (415) 398-3249
TELEEX: 910 277299
INFORMATION FOR SEG ID NO: 40:
SEQUENCE CHARACTERISTICS:
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amino acid
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STATE: California
COUNTRY: United States
ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-398-590A-40
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                                                                                                                                                                                                                                                                                                                         -----YESIKLERHVPYDNS-RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQC 147
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                                                                                                                         55;
                                                                                                                                                                                                                                            52 ---DAGEDSMKVKDEYSDRDENIMKP---EPMGDAEESEMPYSYAREYSD-----
                                                                                 Length 706;
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                                                                                                                         Indels
                                                                                                                                                              S OPTVELKSTERQPLPTESPDALNDYSLPKPHEIENVDSRE---APANEDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
PCT/US95/08429
FILING DATE: 15-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 262.5; DB 3;
; Pred. No. 1.1e-17;
44; Mismatches 111;
                                                                             Query Match 9.7%; Score 265.5; DB 3; Best Local Similarity 27.8%; Pred. No. 5.3e-18; Matches 70; Conservative 39; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14538A-11-1PC
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,680
FILING DATE: 17-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application PC/TUS9508429 GENERAL INFORMATION: APPLICANT:
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TELEFAX: 415-543-5043
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 25.7%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CTCF NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein PCT-US95-08429-5
      protein
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 17 CLASSIFICATION:
HOLECULE TYPE:
PCT-US94-06669-2
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474 KCTSCGSQS----PQHAEMCLHTAGPTFAEEMGETQS------FYSDSSCENGAFFC 520
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                                                                                                                                                                                                                                                                                                                                                                               52 ---DAGEDSMKVKDEYSDRDENIMKP---EPMGDAEESEMPYSYAREYSD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-0594-06669-2
| Sequence 2, Application PC/TUS9406669
| Sequence 2, Application PC/TUS9406669
| Sequence 2, Application PC/TUS9406669
| GENERAL INFORMATION: CLONING AND USES OF THE GENETIC LOCUS TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS TITLE OF INVENTION: Dol-6
| NUMBER OF SEQUENCES: 2
| CORRESPONDENCE ADDRESS: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                        5 QPTVELKSTEEQPLPTESPDALNDYSLPKPHEIENVDSRE---APANEDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06669
                                                                                                                                                                                              Query Match 9.7%; Score 265.5; DB 2; Best Local Similarity 27.8%; Pred. No. 5.3e-18; Matches 70; Conservative 39; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/074,967
FILING DATE: 09-UDN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERA: (212) 664-0525
TELERA: (212) 664-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
                                        : 706 amino acids
amino acid
                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-541B-2
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                                          LENGIH:
                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      521 NECDCRFSEEASLKRHTLQTHSDKP----YKCDRCQASFRYKGNLASHKTVHTGEKPYRC 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCG 207
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                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 ----DAGEDSMKVKDEYSDRDENIMKP---EPMGDAEESEMPYSYAREYSD-----
                                                                                                                                                                                                                                                                                                               Length 706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08553541B
Patent No. 5882858
CENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Chaganti, Raju S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          Indels
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,541B
FILING DATE: MAY 28, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
TELEPHONE: (212) 278-0400
TELERA: (212) 391-0525
TELERA: 42523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Cooper & Dunham LLP
1185 Avenue of the Americas
TELEFAX: (212) 977-9550
TELERAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
TOPOLOGY: linc
                                                                                                                                                                                                                                                                                                           Query Match 9.7%;
Best Local Similarity 27.8%;
Matches 70; Conservative 3
                                                                                                                                                                                                                 : MOLECULE TYPE: protein US-08-074-967-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
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STATE:
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333 TSGELVRHRRYKHTHEKPFKCSMCDYASVEVSKLKRHIRSHTGERPFQCSLCSYASRDTY 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 EGKDVDVSVYDFEEEQQEGLLSEVNAEKVVGNMKPPKPTKIKKKGVKKTFQCELCSYTCP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 ESIKLERHV-PYDNSRPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 KLKRHMRTHSGEKPYECYICHARFTQSGTMKMHILQKHTENVAKFHCPHCDTVIARKSDL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 RRSNLDRHMKSHTDERP----HKCHLCGRAFRTVTLLRNHLNTHTGTRPHKCPDCDMAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 ALTGHLRTHSVEKPYKCEFCGRSYKQRSS-----LEEHKERCRAF------LQNPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----MKPEPMGDAEESEMPYSYAREYSDY---
                                                                                                                                                                                                                                                                                                                                        49; Mismatches 106; Indels 140;
                                                                                                                                                                                                                                                                                Length 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08074967
Patent No. 5641672
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Chaganti, R.S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS TITLE OF INVENTION: bcl-6
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 SLPKPH------EIENVDSREAPANEDEDAGED-----
                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                             Score 266; DB 3
Pred. No. 5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                 7 TVELKSTEEQPL------PTESPDALND--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PACENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0575/43771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 057
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 GDAASVEARHIKAEMGSE 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 G--VHLRKQHSYIEQGKK 468
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                                                              i: 727 amino acids amino acid
                                                                                                                                                                                                                                                                             Query Match 9.8
Best Local Similarity 22.0
Matches 83; Conservative
      INFORMATION FOR SEQ ID NO:
                                     SEQUENCE CHARACTERISTICS
                                                                                                                   TOPOLOGY: Inear
MOLECULE TYPE: protein
PCT-US95-08429-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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CITY: New YORK
STATE: New YOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 RDENI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10112
                                                              LENGTH:
TYPE: am
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-074-967-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 MKVKDEYSDRDEN---IMKPEPMGDAEESEMPYSYAR-----EYSD--YESIKLERHVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- RTENGALAPKQELPSALESHEVPGTLSMGVPQIFKYGETCFPKGRFER--- 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 LHTGEKPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEDIQPTVELKSTEEQPLPTESPDALND -- - YSLPKPHEIENVDSREAPANEDEDAGEDS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 272.5; DB 2; Length 368; 29.6%; Pred. No. 3.8e-19;
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APPLICATION NUMBER: PCT/US95/08429
FILING DATE: 15-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14538A-11-1PC
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF-0356 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
PCT-US95-08429-9
PCT-US95-08429-9
Sequence 9, Application PC/TUS9508429
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CTCF
NUMBER OF SEQUENCES: 21
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
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APPLICATION NUMBER: US 08/261,680
FILING DATE: 17-JUN-1994
September 23, 1997
V: 536
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NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 1453!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Matches 71; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: MMLR?
CLONE: 569710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-933-750C-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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119 CDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 -------RC-RAFLONPDLGDAASVEARHIKAEMGSERALVLDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.0%; Score 273; DB 2; Length 711; 30.0%; Pred. No. 9.6e-19; Live 30; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: LAI, Preeti
APPLICANT: Hallman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Nu-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 NYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKE--
  ZIP: 20037-3202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,170A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERAIING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/08/933,750C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 ASNVAKRKSSMPQKFIGEKRHCFDANY 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            648 --- CGKSFSKKPQLKVHQRIHTGERPY 671
                                                                                                                                                                                   CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELERAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amáno acids
TYPE: amíno acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.09
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-933-750C-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 HQRD----HTEEKPYKCEQCGKGFTRSSSLLIHQAVHTDEK-----PYKCDKCGKGFTRS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 NVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYACQRRDALT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 SSLLIHHAVHTGEKPYKCDKCGKGFSQSSKLHIHQRVHTGEKPYECEECGMSFSQRSNLH 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 GHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERC--------RAFLQNPDLGDA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 ASVEARHIKAEMG------SERALVLDRL------ASNVAKRKSSMPQK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 ----RIHLRVHTGEKPYHCGKCGKGFSQSSKLLIHQRVHTGEKPYECSKCGKGFSQSSNL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 TEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEYSDRDENIM 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%; Score 275.5; DB 2; 25.3%; Pred. No. 3e-19; Live 47; Mismatches 122;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFTCATION: 536
PRIOR APPLICATION DATA:
PPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATORNEY AGENT INFORMATION:
NAME: Billings, Lucy 7, 1825 US REFERENCE/DOCKET NUMBER: 36,749
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 415-845-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.3%
Matches 80; Conservative
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ADDRESSEE: Sughrue, 1
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; CLONE: 641127
US-08-933-750C-17
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REFERENCE/DOCKET NUMBER:
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Best Local S
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                                                                                                                          171 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNP 230
                                                                                                                                                                                   111 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 170
                                                                                                                                                                                                                              DL-GDAASV---EARHIK----AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCF 281
                                                                                                                                                                                                                                                                                         282 DANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVY 341
                                                                                                                                                                                                                                                                                                                                                    342 PIALTRADMPMGAPQEMEKKR-----ILLPEKILPSERGLSPNNSAQDSTDTDSNHE 393
                                                                                                                                                                                                                                                                                                                                                                                                                394 DRQH--LYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452 CDHCHVLFLDYVMFTIHM---GCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR 503
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                                               Length 470;
                                                                            93; Indels
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvil
APPLICANT: Shah, Purvil
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRIES COUNTRIES 21P: 94304
COMPUTER READABLE FORM:
MEDLIM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
TITING DATE: September 23, 1997
                                          44.3%; Score 1208; DB 3;
58.3%; Pred. No. 2.2e-112;
ive 50; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08933750C
Patent No. 5932442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                         Best Local Similarity 58.3 Matches 242; Conservative
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PCT-US95-09345-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 LEEHK------ERC-RAFLQNPDLGDAASVEARHIKAEMGSERALVLDRLASNVA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 LIRHORTHTGERPYACNKCGKAFTQSSHL------IGHQR-----THNRT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MEDIQPTV--ELKSTEEQPLPTE-----SPDAL--NDYSLPKPHEIENVDSREAP 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 ANEDEDAGEDSMKV-----KDEYSDRDENI--MKPEPMGDAEESEMPYSYAREYSDYE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.6%; Score 289.5; DB 2; Length 26.7%; Pred. No. 6.6e-21; Live 49; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Shah, Purviant APPLICANT: Shah, Purviant APPLICANT: Yue, Henry APPLICANT: Yue, Henry APPLICANT: Coejey, Neil C. APPLICANT: Corley, Neil C. TITLE OF INVENTION: HUMAN REGULATORY MOLECULES NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Porter Drive CITY: Palo Alto CONTOURS CALOUR CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS CONTOURS 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GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L. APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillman, Jennifer
Bandman, Olga
                                     TELECOMMUNICATION INFORMATION.
TELEPHONE: 415-855-0555
TELEFRAX: 415-845-4166
                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82; Conservative
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; CLONE: 9337
US-08-933-750C-4
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120 KPFKCHLCNYACRRRDALTGHLRTHSVGKPHKCGYCGRSYKORXSLEEHKERCHNYLESM 179
                                                                                                                                                                                       342 PIALTRADMPMGAPQEMEKKR-----ILLPEKILPSERGLSPNNSAQDSTDTDSNHE 393
                                                                    297 QL---HXXXSXGXPRSNHSAQDXAVXXLLLLSKAKXVXSEREASPSNSCQDSTDTESNXE
                                                                                                                                                                                                                                                                            DL-GDAASV---EARHIK----AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCF
                                                                                                                                      DANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVY
                                                                                                                                                                                                                                                          DRQH--LYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFR
                                                                                                                                                                                                                                                                                                                          Sequence 13, Application PC/TUS9509345
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TILLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: LAHIVE & COCKFIELD
60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Myers, Paul L.
REGIGSTRATION NUMBER: 35,695
REFERENCE/DOCKET WUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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PCT-US95-09345-13
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                                                                             171 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNP 230
              PEKILPSERGLSPNNSAQDSTDTDSNHEDRQH--LYQQSHVVLPQARNGMPLLKEVPRSF 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 30;
                                                                                                                                                                                                                                                                   Sequence 153, Application US/08465590
Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 470;
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58.3%; Pred. No. 2.2e-112;
iive 50; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AscII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FTIING DATE: 05-UNN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Myers, Paul L.
REGISTATION NUMBER: 35,695
REFERENCE/POCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                 481 NMCGYRSHDRYEFSSHIARGEHR 503
                                                                                                                                                                     TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 15
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C-terminal
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Matches 242; Conservative
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November 6, 1999, 09:40:28 ; Search time 15.19 Seconds (without alignments) 381.455 Million cell updates/sec Run on:

US-09-019-348-2 2728 1 MEDIQPTVELKSTEEQPLPT......HDRYEFSSHIARGEHRAMLK 507 Title: Perfect score: Sequence:

BLOSUM62 Scoring table: 119832 segs, 11428610 residues

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AISYLGABAFRPLVQTPPAPTSEMVPVISSVYPIALTRADMP----MGAPQEMEKKRILL 365 | | : | | | : : | | : : | | : : | AINYLGAESLRPLVQTPPG-SSEVVPVISSMYQLHKPPSDGPPRSNHSAQDAVDNLLLS 423

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Sequence 4, Appli Sequence 11, Appl Sequence 2, Appli Sequence 786, Appl Sequence 786, Appl		REGULATORY GENE	3; Length 568; 19; 31; Indels 82; Gaps 18;	STEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEYSDRDENI 71 1 1 1 1 1 1 1 1 1	MKPEPMGDAEESEMPYSYAREYSDYES	IKLERHVPYDNSRPTSGKMNCDVGGLSCISFNVLMVHKRS 138 : :	HTGERPFOCNQCGASFTOKGNLLRHIKLHTGERPFKCHLCNYACORRDALIGHLRTHSVE 198
S-08-102-942A-4 S-08-224-482-11 S-08-946-241B-2 S-08-946-241B-9 S-08-117-952-786 S-08-459-568-2	ALIGNMENTS	3 CELL PATHWAY S 8743	Score 1279; DB 3; Pred. No. 2.5e-119; ; Mismatches 131;	DSREAPANEDEI SGAQQNSKSI	-DAEESEMPYSYAREYSDYES : : LDASGEKMNGSHRDQGSSALSGVGG	TSGKMN :11: GGIRLPNGKLK	TGEKPFKCHLC : SGEKPFKCHLC
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hematopoietic differentiation and a major determinant in lymphocyte differentiation. Other isoforms of Ikaros (see R92016-19) arise from differential splicing of Ikaros gene transcripts. Transgenic animals, esp. mice, having a mutated Ikaros transgene, esp. a mutation that alters the DNA binding domain of the Ikaros protein, are used as models to determine the effects of treatments for immune or nervous system disorders.
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T-cell pathway regulatory gene, Ikaros - encodes family of unique zinc finger proteins, useful for treating immune system disorders Claim 14; Page 41-43; 112pp; English.
The Ikaros gene encodes a zinc finger protein which can be used in a therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is at thisk for an immune disorder. It is of particular use in treating a disorder of the corpus striatum.
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                                                                                                                                                                                                                                                                                                                                        ------MGERPFQCNQSGASFTQKGNLLRH 76
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Murine Ikaros zinc finger protein.
Ikaros; zinc finger; protein; immune disorder; therapy; treatment;
corpus striatum; regulatory gene.
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51.0%; Pred. No. 8.1e-95;
tive 64; Mismatches 94;
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14-SEP-1993; U08743.
14-SEP-1992; US-946233.
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WPI; 94-118387/14.
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                                                              16;
 Length 431;
                        Indels
                          94;
41.9%; Score 1143; DB 1; 50.8%; Pred. No. 1.5e-94;
            Pred. No. 1.5e
65; Mismatches
                        Conservative
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splicing of Ikaros gene transcripts. They are expressed primarily in T cells in the adult and may play a role as a genetic switch regulating entry into the T cell lineage. The invention provides Ikaros nucleic acids (see V42805-11 and V42840), polypeptides (see W7065-17), vectors and host cells. These can be used to treat T and B cell diseases (e.g. immune deficiencies caused by drugs, radiation or cancer), to control expression of heterologous genes placed under control of an Ikaros-responsive element, to treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, amplification or differentiation, especially in haematopoletic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences.
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15-FEB-1996.
28-JUL-1995; U09345.
29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
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WPI; 96-129389/13.
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N-PSDB; T16059
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To control cell differentiation

Disclosure: Page 59-60: 158pp; English.

This is an example of a potential Tkaros sequence derived from a degenerate library of polypeptides based on the amino acid sequences of human and murine Ikaros isoform i proteins hik-1 (see W70964) and mik-1 (see W70966). A combinatorial library is produced using a degenerate library of genes which each include the fast a portion of potential Ikaros sequences. It can be generated by combinatorial library is generated by combinatorial mit the early stages of lymphocyte differentiation. Different isoforms arise from differential
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(GEHO ) GEN HOSPITAL CORP.
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02-JAN-1997; 194256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc_difference 432
 Misc_difference 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georgopoulos K;
WPI; 98-378292/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc_difference
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111 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 170
                                                                                                                    60 RLPNGKLKCDICGIXCIGPNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHSGE 119
                                                                                                                                                                                                             120 KPFKCHLCNYACRRRDALTGHLRTHSVGKPHKCGYCGRSYKQRXSLEEHKQRCHNYLESM 179
                                                                                                                                                                                     KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNP 230
                                                                                                                                                                                                                                                                                 DL-GDAASV---EARHIK----AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCF 281
                                                                                                                                                                                                                                                                                                                                                                                              PIALTRADMPMGAPQEMEKKR-----ILLPEKILPSERGLSPNNSAQDSTDTDSNHE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 QL---HXXXSXGXPRSNHSAQDXAVXXLLLSKAKXVXSEREASPSNSCQDSTDTESNXE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRQH--LYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 EQRSGLIYLTNHIX--XXAXXXXXLKEEXRAYXXLRAASENSQDAXRVVSTSGEQXKVYK 411
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine Ikaros protein mIk-2. Ikaros; transgenic mouse; lymphocyte; immunocomprised; immune system disorder; nervous system disorder; animal model; mIk-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders Disclosure; Fig 1: 102pp; English.

The sequence of 48 kpa mouse Ikaros protein mIK-2 (R92014) was deduced from mouse Ikaros cDNA (T16059) isolated from a mature T-cell line E15 library. Ikaros protein is a master regulator of
                                                                                                                                                                                                                                                                                                                                                                          DANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 CDHCHVLFLDYVMFTIHM----GCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
  Length 470;
                                             Indels
44.2%; Score 1205; DB 1;
58.1%; Pred. No. 4.7e-100;
iive 51; Mismatches 93;
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Mus sp.
                                                   RESULT
W70970
 g
                                                                                                   system or corpus striatum

Striatum 127-130; 111pp; English.

The present invention describes a purifiled peptide having at least one coffus invention describes a purifiled peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFKB element or an itaros binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFKB element or an itaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring itaros isoform to any of a delta A element, an NFKB element or an itaros binding oligonucleotide consensus sequence; (d) it competitively inhibits its faros binding to itaros responsive elements; or (e) it inhibits protein protein interactions of transcriptional complexes formed with naturally occurring itaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFKB elements and/or itaros-binding oligonucleotides, bind to delta A elements, NFKB elements and/or itaros-binding oligonucleotides, competitively inhibit inatos binding to itaros-responsive elements and/or itaros inhibit protein-protein interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competitively inhibit interactions of transcriptions competities, competities competities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AlDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence represents an Ikaros protein general formula from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QL---HXXXSXGXPRSNHSAQDXAVXXLLLLSKAKXVXSEREASPSNSCODSTDTESNXF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQRSGLIYLTNHIX--XXXXXXXXKREXRAYXXLRAASENSQDAXRVVSTSGEQXKVYK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRQH--LYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 DL-GDAASV---EARHIK----AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 PIALTRADMPMGAPQEMEKKR-----ILLPEKILPSERGLSPNNSAQDSTDTDSNHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVY
                                                                                                                                                                                                                                                   Ikaros poly:peptide(s) - useful for treating disorders of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDHCHVLFLDYVMFTIHM---GCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.3%; Score 1208; DB 1;
58.3%; Pred. No. 2.5e-100;
ive 50; Mismatches 93;
/note= "any amino acid"
                                note- "any amino acid"
                                                               'note= "any amino acid"
                                                                                                                                                14-SEP-1992; US-946233.
14-SEP-1993; US-121438.
05-JUN-1995; US-465590.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 58.3%
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-238212.
US-946233.
US-121438.
                                                 Misc_difference 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 AA;
                                                                                                                                                                                                                 Georgopoulos K;
WPI; 98-582621/49.
                 Misc_difference
                                                                                                                                    02-MAY-1994;
                                                                                                                 05-JUN-1995;
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/note= "the codon for Thr-89 may be made degenerate to provide a stop codon in recombinant genes of a degenerate library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "the codon for Ser-145 may be made degenerate to provide a stop codon in recombinant genes of a degenerate library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "the codon for Pro-187 may be made degenerate to provide a stop codon in recombinant genes of a degenerate library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "the codon for Gly-232 may be made degenerate to provide a stop codon in recombinant genes of a degenerate library"
412 CEHCRVLFLDHVMYTIHMXXXGCHGFRDPFECNMCGYHSQDRYEFSSHITRGEHR 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Gly, Ala, Val, Ile, Leu, Ser, Thr
/note= "residue 184 may also not be present"
Misc_difference 185
                                                                                                                             11-JAN-1999 (first entry)
Ikaros isoform 1 consensus.
Ikaros, mIK-1; hIK-1; transcription factor; mouse; human; Iymphocyte; call differentiation; T cell; cancer; immunodeficiency; Alzheimer's disease; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                            label- Gly, Ala, Val, Ile, Leu, Ser, Thr
                                                                                                                                                                                                                                                Location/Qualifiers
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Misc_difference 187
                                                                                                                                                                                                                                                                                     'note- "variable"
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                                                                                             W70970 standard; Protein; 470 AA.
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Misc_difference 196
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                                                                                                             W70970;
11-JAN-1999
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Misc_difference 432
 11;
The sequence of an Irva, Lugup; English.

specification. Ikaros protein (19201) is provided in the specification. Ikaros protein is a master regulator of hematopoietic differentiation and a major determinant in lymphocyte differentiation. Isoforms of Ikaros (see 192014-19) arise from differential splicing of Ikaros gene transcripts. Transgenic animals, pref. mice, having a mutated Ikaros transgene, esp. a mutation that models to determine the effects of treatments for immune or nervous system disorders.
                                                                                                                                                              393
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-1999 (first entry)
Ikaros protein general formula.
CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS;
Alzheimer's disease.
                                                                                                                                    Gaps
                                                                                                                                                    111 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 170
                                                                                                                                                                                       KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNP 230
                                                                                                                                                                                                DL-GDAASV---EARHIK----AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCF 281
                                                                                                                                                                                                                                                               341
                                                                                                                                                                                                                                                                               296
                                                                                                                                                                                                                                                                                                                                     451
                                                                                                                                                                                                                                                                                                                                                      411
                                                                                                                                                                                                                                                                                                 PIALTRADMPMGAPQEMEKKR-----ILLPEKILPSERGLSPNNSAQDSTDTDSNHE
                                                                                                                                                                                                                                                                                                                   QL---HXXXSXGXPRSNHSAQDXAVXXLLLLSKAKXVXSEREASPSNSCQDSTDTESNXE
                                                                                                                                                                                                                                                                       EQRSGLIYLTNHIX--XXAXXXXXKREEXRAYXXLRAASENSQDAXRVVSTSGEQXKVYK
                                                                                                                                                                                                                                   DANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVY
                                                                                                                                                                                                                                                                                                                                    DRQH--LYQQSHVVLPQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFR
                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                        CDHCHVLFLDYVMFTIHM --- GCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR
                                                                                                                  Length 470;
                                                                                                                                   Indels
                                                                                                                                   93;
                                                                                                                 44.3%; Score 1208; DB 1;
58.3%; Pred. No. 2.5e-100;
tive 50; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "any amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "any amino
Misc_difference 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino
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                                                                                                                         Best Local Similarity 58.39
Matches 242; Conservative
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-MAR-1994

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Georgopoulos K;
WPI; 96-129389/13.
WPIs 96-129389/13.
Stransgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders
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note= "unidentified amino acids"
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misc_difference 352
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                                                                     'note- "unidentified amino
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   Location/Qualifiers
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29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 170
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                                                                                                                                                                                                                                                                                                                                   T-cell pathway regulatory gene, Ikaros - encodes family of unique zinc finger proteins, useful for treating immune system disorders claim 14: Page 44-46; 112pp; English.

The Ikaros gene encodes a zinc finger protein which can be used in a therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is at risk for an immune disorder. It is of particular use in treating a Sequence 537 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte;
umnunocomprised; immune system disorder; nervous system disorder;
                             21-OCT-1994 (first entry)
Peptide with Ikaros protein activity.
Ikaros; zinc finger; protein; immune disorder; therapy; treatment; corpus striatum; regulatory gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |: |||||||||: :||||||||: |DPYDSA-TYEKENEMMKSHVMDQAINNAINYLGAESLRPLVQTPPG-GSEVVPVISPMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                                                                                                                                                          encoded by a stop codon in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.4%; Score 1265.5; DB 1; Length 537; 60.8%; Pred. No. 2.1e-105;
Live 60; Mismatches 71; Indels 31;
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                                                                                                                                                        /note= "Position is encoded by a str
corresponding nucleotide sequence."
                                                                                                                       Location/Qualifiers
standard; Protein; 537 AA
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09-MAY-1996 (first entry)
Ikaros protein.
                                                                                                                                                                                                                            14-SEP-1993; U08743.
14-SEP-1992; US-946233.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 251; Conservative
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N-PSDB; 044980.
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                                                                                                       Homo sapiens.
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Query Match

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                                                                                                                                                             Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders.

Transgenic rodent for immune and nervous system disorders of selects of treatment for immune and nervous system disorders.

Disclosure; Fig 2, 102pp; Bnglish.

Chan almost full-length CDNA sequence (716060) codes for part (R92015) of the human Ikaros protein, a zinc finger protein that is a master regulator of haematopoietic differentiation and amjor cherminant in lymphocyte specification and development. Different isoforms (see R92014 and R92016-19) of mouse Ikaros been isolated. Transgenc animals, pref. mice, having a mutated Ikaros transgenc, esp. a mutation that alters the DNA binding domain of the Ikaros protein, are used as models to determine the effects of treatments for immune or nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                      111 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 KPFKCHLCNYACORRDALTGHLRTHSVEKPYKCEFCGRSYKORSSLEEHKERCRAFLONP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DL-GDAASV---EARHIK----AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCF 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 DRQH--LYQQSHVVLPQARNGMPL-LKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVF 450
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                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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immunocomprised; immune system disorder; nervous system disorder;
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                                                                                                                                                                                                                                                                                                                                                                          Length 461;
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                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                      46.8%; Score 1276.5; DB 1
61.3%; Pred. No. 1.7e-106;
iive 60; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W72672 standard; Protein; 461
 Human Ikaros protein hIk-1.
                                                                           15-FEB-1996.
28-JUL-1995; U09345.
29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.34
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease.
                                                                                                                           Georgopoulos K;
WPI; 96-129389/13.
N-PSDB; T16060.
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US5824770-A.
                                                              WO9604372-A1
                                                     sapiens
                                       animal model
                                                                          15-FEB-1996
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The present invention describes a purified peptide having at least one system or corpus striatum

Striam or corpus striatum

Claim 1: Column 55-58; 111pp; English.

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFKB element or an Ixaros binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFKB element or an Ixaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ixaros binding to Ixaros responsive element; an NFKB element or an Ixaros binding oligonucleotide consensus sequence; (d) it competitively inhibits Ixaros binding to Ixaros responsive elements; or (e) it inhibits protein protein interactions of transcriptional complexes formed with naturally occurring ixaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFKB elements and/or Ixaros binding oligonucleotides, competitively inhibit binding of naturally occurring to Ixaros responsive elements and/or competitively inhibit Ixaros binding to Ixaros-responsive elements and/or inhibit protein-protein interactions of transcriptions of transcriptions of transcriptions of transcriptions of transcriptions of transcriptions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence represents a specifically claimed human Ikaros protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIALTRADMPMGAPQE------MEKKRILLPEKILPSERGLSPNNSAQDSTDTDSNHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 DRQH--LYQQSHVVLPQARNGMPL-LKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DL-GDAASV---EARHIK----AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQRSGLIYLINHI----ARRAQRVSLKEEHRAYDLLRAASENSQDALRVVSTSGEOMKVY
                                                                                                                                                                                                                                                                                                                               - useful for treating disorders of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 RCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.8%; Score 1276.5; DB 1
61.3%; Pred. No. 1.7e-106;
live 60; Mismatches 69;
                                                            14-SEP-1992; US-946233.
14-SEP-1993; US-121438.
05-JUN-1995; US-465590.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 61.3
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                           poly:peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                       98-582621/49.
                                                                                                                                                                                                                                                                                         N-PSDB: V66969
                                                                                                                                                                                                                        Georgopoulos
05-JUN-1995;
02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                               Ikaros
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S

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12;
This is the amino acid sequence of human Ixaros protein isoform

"Ik1, deduced from a cDNA clone (see V42806) obtained from a
Jurkat T cell line cDNA library. Native Ixaros is active in the
early stages of lymphocyte differentiation, binding to and
activating the CD3-delta gene enhancer (see V42804)

"Cof the human Ixaros family (see also W7096) and W70971) are
isoforms that arise from differential splicing of Ixaros gene
transcripts, and contain differential splicing of zinc fingers.

"They are expressed primarily in T cells in the adult and may play a
role as a genetic switch regulating entry into the T cell lineage.

The human and murine sequences (see also W70963 and W70965-68) are
very similar. The invention provides Ixaros nucleic acids, vectors
and host cells expressing Ixaros polypeptides. These can be used
to treat T and B cell diseases (e.g. immune deficiencies caused by
curys, radiation or cancer), to control expression of heterologous
genes placed under control of an Ixaros-responsive element, to
treat nervous system diseases (e.g. Alzheimer's disease) and to
the human cell of division, amplification or differentiation, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : |:: | |: | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 RPTSGKMNCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 KPFKCHLCNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DANYNPGYMYEKENEMMQTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVY 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIALTRADMPMGAPQE------MEKKRILLPEKILPSERGLSPNNSAQDSTDTDSNHE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::: :| :|: || : || | : ||| ||::||:
EQRSGLIYLINHI----ARRAQRVSLKEEHRAYDLLRAASENSQDALRVVSTSGEQMKVY 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-077-1994 (first entry)
Ikaros zinc finger protein isoform IK-1.
Ikaros; zinc finger; protein; immune disorder; therapy; treatment; corpus striatum; regulatory gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DL.GDAASV---EARHIK-----AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRQH--LYQQSHVVLPQARNGMPL-LKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in haematopoietic cells. Some Ikaros isoforms are antagonistic others and may be used to inhibit interaction with DNA sequences. Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.9%; Score 1279.5; DB 1; Length 461; 61.5%; Pred. No. 9.4e-107; ive 59; Mismatches 69; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCDHCHVLFLDYVMFTIHMGCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .. .53
'label= Exons 1/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥.
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/label= Exon 4.
248. .288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exon 3.
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R46965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 61.54
Matches 254; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54. .141
/label= E
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                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                          STEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEYSDRDENI 71
                                                                                                                                                                                                 be used in
                                                                                                                                         WPI: 94-118387/14.

T-cell pathway regulatory gene, Ikaros - encodes family of unique T-cell pathway regulatory gene, Ikaros - encodes family of unique Ciaim [14]. Figure 4: 112pp; English.

The Ikaros gene encodes a zinc finger protein which can be used in therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is risk for an immune disorder. It is of particular use in treating disorder of the corpus striatum.
                                                                                                                                                                                                                                                                                                                                                                         PNVLMVHKRSHTGERPFQCNQCSSALSGVGGIRLPNGKLKCDICGIVCIGPNVLMVHKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RALVLDRLASNVAKRKSSMPQKFIGEKRHCF-DANYNPGYMYEKENEMMQTRMMDQAINN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIGERPFOCNOCGASFTOKGNLLRHIKLHIGEKPFKCHLCNYACQRRDALIGHLRTHSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPYKCEFCGRSYKQRSSLEEHKERCRAFLQN---PDLGDAASVEARHIK----AEMGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEKILPSERGLSPNNSAQDSTDTDSNHEDRQH--LYQQSHVVLPQARNGMPLLKEVPRSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 KAKSVSSEREASPSNSCQDSTDTESNAEEQRSGLIYLTNH-INPHARNGL-ALKEEQRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHM---GCHGFRDPFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TSGKMNCDVCGLSCISFNVLMVHKRS
                                                                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                                                                                         Length 568;
                                                                                                                                                                                                                                                                                                      46.9%; Score 1279; DB 1; Length 50 49.4%; Pred. No. 1.4e-106; Live 72; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             72 MKPEPMG------DAEESEMPYSYAREYSDYES-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.
                       ė.
'n
                                                 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --IKLERHVPYDNSRP-----
           289. .333
/label= Exon 6
334. .568
/label= Exon 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R92015 standard; Protein; 461
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/label = Exon
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09-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 49.4%
Matches 278; Conservative
                                                                                                   14-SEP-1992; US-946233.
(GEHO ) GEN HOSPITAL CORP.
                                                                        31-MAR-1994.
14-SEP-1993; U08743.
                                                                                                                                  Georgopoulos K
                                                             W09406814-A
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STEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEYSDRDENI 71
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This is the amino acid sequence of murine Ikaros protein isoform mix-1, deduced from a cDNA clone (see V42808) obtained from a contact of the first is the amino acid sequence of murine Ikaros is active mature murine T cell line El4 library. Native Ikaros is active in the early stages of lymphocyte differentiation, binding to and activating the CD3-delta gene enhancer (see V42804). Proteins of the murine Ikaros family (see also W70953 and W7095-68) are isoforms that arise from differential splicing of Ikaros gene transcripts, and contain different combinations of zinc fingers. They are expressed primarily in T cells in the adult and may play a cole as a genetic switch regulating entry into the T cell lineage. The murine and human sequences (see W70964, W70965 and W7091) are very similar. The invention provides Ikaros nucleic acids, vectors and host cells expressing Ikaros polypeptides. These can be used to treat T and B cell diseases (e.g. immune deficiencies caused by drugs, radiation or cancer), to control expression of heterologous genes placed under conter), to control expression of heterologous
                           treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, amplification or differentiation, especially in haematopoietic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences. Sequence 518 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and to control cell differentiation
           PQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFT
                                                                                                                                                                                                                                            Ikaros; mIK-1; transcription factor; mouse; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis.
                                                                                        467 IHM --- GCHGFRDPFECNMCGYRSHDRYEFSSHIARGEHR
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="zinc finger motif"
460. 480
/note="zinc finger motif"
491. 613
/note="zinc finger motif"
                                                                                                                                                                                                                                                                                                                                                  147. .167
/note= "zinc finger motif"
175. .195
                                                                                                                                                                                                                                                                                                                         119. .139 //note= "zinc finger motif"
                                                                                                                                                                                                                                                                                                                                                                                                       "zinc finger
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                W70966 standard; Protein; 518 AA
                                                                                                                                                                                                                                                                                                                                                                               203
                                                                                                                                                                                                             11-JAN-1999 (first entry)
Mouse Ikaros isoform mIk-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JAN-1997; 194256.
05-SEP-1996; US-711417.
(GEHO ) GEN HOSPITAL CORP.
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Nev By 198-378296.

New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and to control cell differentiation claim 7; Page 70-72; 158pp; English.
EARHIK - - - - - AEMGSERALVLDRLASNVAKRKSSMPQKFIGEKRHCF-DANYNPGYMYE
                                                                                                                                                                                                                                                     242 FINHNEWAEDLCKIGAERSLYLDRIASNVAKRKSSMPQKFLGDK--CLSDMPYDSA-NYE
                                                                                                                                                                                                                                                                                                                     357 RSNHSAQDAVDNLLLESKAKSVSSEREASPSNSCQDSTDTESNAEEQRSGLIYLTNH-IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 RACEMNGEECAEDLRMLDASGEKMNGSHRDQGSSALS-----GVGGIRLPNGKLKCDI
                                                                                                         CGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYA
                                                                                                                                                                      CQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNPDLGDAASV---
                                                                                                                                                                                                                                                                                                    293 KENEMMOTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVYPIALTRADMP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ikaros; hIK-1; transcription factor; human; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis.
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/note= "zinc finger motif"
120. .140
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/note= "zinc finger motif"
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05-SEP-1996; US-711417.
(GEHO ) GEN HOSPITAL CORP.
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WPI; 98-378292/33.
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17;

Gaps

46;

47.1%; Score 1284; DB 1; Length 518; 53.3%; Pred. No. 4.4e-107; Live 68; Mismatches 129; Indels 4

Conservative

Query Match Best Local Similarity Matches 277; Conserv

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Page

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differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---MGAPQEMEKKRILLPEKILPSERGLSPNNSAQDSTDTDSNHEDRQH--LYQQSHVVL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQARNGMPLLKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure: Fig 4; 102pp; English.

The sequence of 57.5 kDa mouse Ikaros protein mIK-1 (R92017) was deduced from mouse Ikaros protein miK-1 (R92017) was reclused from mouse Ikaros protein is a master regulator of hematopoietic differentiation and a major determinant in lymphocyte differentiation. Other isoforms of ikaros (see R92014, R92016 and R92018-19) arise from differential splicing of Ikaros gene transcripts. Transgenc animals, esp. mice, having a mutated Ikaros transgenc, esp. a mutation that alters the DNA binding domain of the Ikaros protein, are used as models to determine the effects of Sequence 518 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNYA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse Ikaros mlk-1.
CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                          DAEESEMPYSYAREYSDYESIKLERHVPYDNSRPTSGKMNCDV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                69 RACEMNGEECAEDLRMLDASGEKMNGSHRDQGSSALS-----GVGGIRLPNGKLKCDI 121
                                                                                                                                                                                                                                                                                                                                                          12 STEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEYSDRDENI 71
                                                                                                                                                                                                                                                                                                                                                                         Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNPDLGDAASV---
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53.3%; Pred. No. 4.4e-107;
tive 68; Mismatches 129;
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                                  29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
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                      28-JUL-1995; U09345.
                                                             Georgopoulos K;
WPI; 96-129389/13.
                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 277; Conserv
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                                                                                    N-PSDB; T016062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 CORRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNPDLGDAASV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KENEMMOTRMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVYPIALTRADMP-
                                                                                                                                                                                             - useful for treating disorders of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
marker; immune system; corpus striatum; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.1%; Score 1284; DB 1; 53.3%; Pred. No. 4.4e-107;
                                                  20-OCT-1998.
05-JUN-1995, 465590.
02-MXY-1994; US-238212.
14-SEP-1992; US-946233.
14-SEP-1993; US-121438.
05-JUN-1995; US-465590.
(GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                                            Ikaros poly:peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                      Georgopoulos K;
WPI; 98-582621/49.
                                                                                                                                                                               N-PSDB; V66971
           Alzheimer's
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516 AA;

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Sequence
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This is the amino acid sequence of human Ikaros protein isoform

Int.1, deduced from a CDNA clone (see V42840) obtained from a

Uurkat T cell line CDNA library. Native Ikaros is active in the
early stages of lymphocyte differentiation, binding to and
activating the CD3-delta gene enhancer (see V42804). Proteins

of the human Ikaros famniy (see also W70054 and W70059) are
isoforms that arise from differential splicing of Ikaros gene
transcripts, and contain different combinations of zinc fingers.

They are expressed primarily in T cells in the adult and may play a

role as a genetic switch regulating entry into the T cell lineage.

They are expressed primarily in T cells in the adult and may play a

role as a genetic switch regulating entry into the T cell lineage.

The human and murine sequences (see also W70965 and W70965-68) are

very similar. The invention provides Ikaros nucleic acids, vectors
and host cells expressing Ikaros polypeptides. These can be used
to treat T and B cell diseases (e.g. immune deficiencies caused by

drugs, radiation or cancer), to control expression of heterologous
genes placed under control of an Ikaros-responsive element, to

treat nervous system diseases (e.g. Alzheimer's disease) and to

modulate cell division, amplification or differentiation, especially
in haematopoietic cells. Some Ikaros isoforms are antagonistic of
others and may be used to inhibit interaction with DNA sequences.
                                                                                                             480
               KRILLPEKILPSERGLSPNNSAQDSTDTDSNHEDRQHLYQQSHVVLPQARNGMPLLKEVP 420
                                                                                 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentiation of lymphocytes - existing in several isotorms, and related products, used to treat e.g. immune diseases or cancer and to control cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and
RMMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVYPIALTRADMPMGAPQEMEK
                                                                   RSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHVLFLDYVMFTIHMGCHGFRDPFEC
                                                                                                                                                                                                                                                                                                   Human Ikaros isoform hik-1.
Ikaros; hIK-1; transcription factor; human; lymphocyte; cell differentiation; T cell; cancer; immunodeficiency; Alzheimer's disease; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                              /note= "zinc finger motif"
147. .167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "zinc finger motif"
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461. .481
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                                                                                                                                                                NMCGYRSHDRYEFSSHIARGEHRAMLK
                                                                                                                                                                                                                                                            W70971 standard; Protein; 516
                                                                                                                                                                                                                                                                                           (first entry)
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02-JAN-1997; 194256.
05-SEP-1996; US-711417.
(GEHO ) GEN HOSPITAL CORP.
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489. .511
/note= "zi
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203. .2
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WPI: 98-378292/33.
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                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                        64
                                                                      8 VELKSTEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKVKDEYSDR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte;
immunocomprised; immune system disorder; nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 KCDICGIICIGPNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHSGEKPFKCHL
                                                                                                                                                                                                                                                                                                 DMPMGAPQE-----MEKKRILLPEKILPSERGLSPNNSAQDSTDTDSNHEDRQH--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 MSFSSGKESPPVSDTPDE-GDEPMPIPEDLSTTSGGQGSSKSDRVVASN---VKVETQSD
                                                                                                                                                                                                           118 NCDVCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHL
                                                                                                                                                                                                                                                                               CNYACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNPDL-GDAA
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                                                                                                                                                                                                                                                                                                                                                                                                                     289 YMYEKENEMMQTRWMDQAINNAISYLGAEAFRPLVQTPPAPTSEMVPVISSVYPIALTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 YQQSHVVLPQARNGMPL-LKEVPRSFELLKPPPICLRDSIKVINKEGEVMDVFRCDHCHV
                                     52;
 Length 516;
                                     Indels
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47.7%; Score 1302; DB 1;
52.3%; Pred. No. 1.1e-108;
tive 75; Mismatches 124;
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147. 167
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fnote= "zinc finger domain F5"
igl. .513
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                     Similarity
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/note= "zinc finger domain F6"

The zif268-zif268 TRP-1 protein. DNA

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9.4

256.5 253

44

ALIGNMENTS

Compugen Ltd GenCore version 4.5 Copyright (c) 1993 - 1998 Comp

sw model using protein search, OM protein

(without alignments) 565.655 Million cell updates/sec November 6, 1999, 06:53:38; Search time 21.23 Seconds US-09-019-348-2 2728 1 MEDIQPTVELKSTEEQPLPT......HDRYEFSSHIARGEHRAMLK 188963 segs, 23686106 residues **BLOSUM62** Scoring table: score: Database : Searched: Sequence: Perfect Run on:

A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ikaros protein. Tr Ikaros protein gen Ikaros isoform i c Murine Ikaros prot Murine Ikaros zinc Murine Ikaros mik-Mouse Ikaros isofo Human Aiolos polyp Ikaros protein. Tr Ikaros isoform. Ik Ikaros protein SEO Ikaros protein SEO Ikaros protein SEO Ikaros protein SEO Mouse Ikaros mīk-4 Mouse Ikaros isofo Murine Ikaros prot Mouse Ikaros mik-3 Mouse Ikaros isofo Mouse Ikaros isofo Mouse Aiolos polyp Human Ikaros isofo Mouse Ikaros mīk-1 Mouse Ikaros isofo Human Ikaros prote Human Ikaros. Ikar Mouse Ikaros mík-5 Ikaros protein SEQ Ikaros protein SEQ Human BRCAl-associ Human OTK18. Novel Human Ikaros isofo Peptide with Ikaro Human Ikaros prote Murine Ikaros prot Human SRE-ZBP anal Murine Ikaros prot Ikaros zinc finger Murine Ikaros W72677 W70969 R92018 W72675 W70967 W70965 W70968 R92019 W70964 R46965 R92015 W72672 R46964 W70963 W15575 R92017 W72674 W70966 W72678 W70970 R92014 R92020 R92016 W72676 W72673 R46963 W72681 Query Match Length 1143 1020.5 1020.5 1020.5 999.5 999.5 1302 1284 1284 1284 1279.5 1279 1276.5 1276.5 1276.5 1276.5 671 671 600 588.5 537.5 537.5 313 313 313 303 273.5 27 Score Result

Indimugantana Amministration Aministration Amministration Amminist Aiolos polypeptide and corresponding DNA - used to reconstitute a mammalian immune system, for the treatment of T cell leukaemia(s) /note= "conserved activation domain of Aiolos" Mouse Aiolos polypeptide. Aiolos; transcription activator; immune system; T lymphocyte; B lymphocyte; leukaemia; lymphoma; asthma; gene therapy; 290. .344
/label= Activation_domain Location/Qualifiers W15574 standard; Protein; 507 AA. W15574; 17-0CT-1996; U16774. 18-0CT-1995; US-005529. 14-MAY-1996; US-017646. (GEHO) GEN HOSPITAL CORP. Georgopoulos K, Morgan BA; 07-JUL-1997 (first entry) Georgopoulos K, Mc WPI; 97-245047/22. cransgenic animal. N-PSDB; T60490. NO9714714-PT Query Match domain Mus sp RESULT W15574

61 KDEYSDRDENIMKPEPMGDAEESEMPYSYAREYSDYESIKLERHVPYDNSRPTSGKMNCD 120 Gaps 1 MEDIQPTVELKSTEEQPLPTESPDALNDYSLPKPHEIENVDSREAPANEDEDAGEDSMKV 121 VCGLSCISFNVLMVHKRSHTGERPFQCNQCGASFTQKGNLLRHIKLHTGEKPFKCHLCNY ACQRRDALTGHLRTHSVEKPYKCEFCGRSYKQRSSLEEHKERCRAFLQNPDLGDAASVEA 99.9%; Score 2724; DB 1; 99.8%; Pred. No. 2.5e-236; tive 0; Mismatches 1; Matches 506; Conservative Similarity Local 61 181 241 g g ö g à ά 셤 ογ

241

Myc-binding zinc-f Zif268-Zif268 zinc

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ö Gaps ; 0 Query Match
4.2%; Score 84; DB 38; Length 356;
Best Local Similarity 73.0%; Pred. No. 1.8e-10;
Matches 108; Conservative 0; Mismatches 40; Indels

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Search completed: November 6, 1999, 08:16:48 Job time: 501 sec

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Mus musculus
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: esfewatson.wustl.edu
High quality sequence stops: 257
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: M13RPI
760 caacgittigaiggittcataagcgaagccataccggcgaacgcccgittccagigtaatca 819
                                                                               H83408 355 bp mRNA EST 13-NOV-1995 ys90h12.rl Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222119 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 353)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikfin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                        /tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project
Unpublished (1995)
On Jan 24, 1995 this sequence version replaced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="cDB:3850880"
/db_xref="taxon:9606"
/map="l7; 17p11.2-p13; 17p12-17p13"
/clone="IRAGE:222119"
/clone=lib="Soares retina N2b5HR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l. .355
/organism="Homo sapiens"
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H83408.1 GI:1062079
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                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                human.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 356)
Marra, M., Hillier, Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA764246 356 bp mRNA EST 27-JAN-1998 vv49e05.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1225760 5' similar to TR:013100 013100 IKAROS HOMOLOG;, mRNA sequence.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                            824 ggggcatcttttactcagaaaggtaacctcctccgtcatattaaactgcacacgggggaa 883
                                                                                                                                                                                                                                                            764 gtcttgatggttcataagcgaagccataccggcgaacgcccgttccagtgtaatcagtgc 823
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
On May 8, 1995 this sequence version replaced gi:801088
                                                                                                                                                        Length 355;
  constructed
                                                                                                                                                                                                           Indels
                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
Library (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: -28m13 rev2 ET from Amersham
                                                                                                                                                      Score 85.2; DB 24
Pred. No. 9.5e-11;
0; Mismatches 93
  University of Toronto. Libra
Soares and M.Fatima Bonaldo.
67 c 88 g 69 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares 2NbMT" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1225760"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Thymus"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA764246.1 GI:2811768
                                                                                                                                                        4.3%;
                                                                                                                                                                                                           Conservative
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                 AA808413 339 bp mRNA EST 19-FEB-1998 oa43h06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1307771 3's similar to TR:000598 000598 HIK1. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 339) NCI-GGAP http://www.ncbi.nlm.nih.gov/nciegap. NCI-GGAP http://www.ncbi.nlm.nih.gov/nciegap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
ggaagaagctacaagcagagaagctccctggaggagcacaaggaacgctgccgagctttt 1051
                       On Jan 19, 1998 this sequence version replaced gi:2153413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 295.
Location/Qualifiers
1. 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1307771"
/clone_lib="NCI_CGAP_GCBI"
                                                                             1052 cttcagaaccctgacctgggggacgctg 1079
                                                                                                    92877819
AA808413.1 GI:2877819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                RESULT 13
AA808413/c
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                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
992
                                                                                                                                                                                                                                                                                ACCESSION
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SOURCE
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                                                                         AI428749 479 bp mRNA EST 09-MAR-1999 vv49e05.yl Soares 2NbMT Mus musculus cDNA clone IMAGE:1225760 5' similar to TR:042244 042244 IKAROS-RELATED TRANSCRIPTION FACTOR;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Jases 1 to 479)

Mara, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Widerwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., The WashU-NcI Mouse EST Project 1999

Unpublished (1999)

On Mar 16, 1998 this sequence version replaced gi:2961771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TTE1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 87.2; DB 46; Length 479;
Pred. No. 3.6e-11;
0; Mismatches 38; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40RP from Gibco
High quality sequence stop: 459.
Location/Qualifiers
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AI428749.1 GI:4274675
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Best Local Similarity 74.3
Matches 110; Conservative
                                                                                                                                      mRNA sequence.
AI428749
                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                        house mouse.
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ORIGIN
                                   RESULT 12
                                                                                                                                                                                                                                                         ORGANISM
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JOURNAL
COMMENT
                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                   KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                      AI428749
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                                                                                                                                      Length 339;
                                                                                                                                                     Indels
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                      Score 86.8; DB 38;
Pred. No. 3.8e-11;
0; Mismatches 52;
                                                                                                                                      Query Match
Best Local Similarity 69.4%;
Matches 118; Conservative
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COMMENT

FEATURES

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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

L (bases 1 to 557)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: placenta; Vector: pr7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in t correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      700 cagcagaccaaccagtgggaagatgaactgcgacgtgtgcgggttatcctgcattagctt 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 CATTCGACTTCCTAACGGAAAACTAAAGTGTGATATCTGTGGGATCGTTTGCATCGGGCC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          760 caacgtcttgatggttcataagcgaagccatacoggcgaacgcccgttccagtgtaatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 CAATGTGCTCATGGTTCACAAAAGAAGTCATACTGGTGAACGGCCTTTCCAGTGCAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              placenta 4NbMP13.5 14.5"
                                                                                                                                                                                                                             Unpublished (1996)
On Jan 17, 1998 this sequence version replaced gi:1900564
                                                                                                                                                                                                                                                                                                                                                                   63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 45; Length 557;
                                                                                                                                                                                                                                                                                                                 WashU HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
111 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 113.6;
70.4%; Pred. No. 1.7e
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                 Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40RP from Gibco
High quality sequence stop: 417.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:459676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                      Waterston, R.
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Matches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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       ORGANISM
                                                                                                                                                                                                        TITLE
JOURNAL
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                                                                        REFERENCE
                                                                                             AUTHORS
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                                                                                                                                                                                                                                                       COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 54 c 60 g 43 t
                                                                                                                                                                            DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1727 tgtgaccactgccacgtcctcttcctagattatgtgatgttcaccatccacatggggtgc 1786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1607 gggatgcctcttctgaaggaggtccctcgctcttttgaactcctcaagcccctcccatc 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                  Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jan 17, 1998 this sequence version replaced gi:2045300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 154.6; DB 41; Length 217;
Pred. No. 1.5e-27;
0; Mismatches 39; Indels 0;
                                                                                                                  Σ.
                                                                                 Email: Robert Strausbergenih, gov
CDNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.
                                                                                                                                                          CDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                          Insert Length: 437 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                  www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                          Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                          1. .217
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="18"
                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
/lab_host="DH10B"
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VERSION KEYWORDS

SOURCE

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/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA866707 936 bp mRNA EST 16-MAR-1998 vx85a10.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1281978 5'similar to 9b:L03547 Mouse Ikaros DNA binding protein (MOUSE);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
MGI:673778
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 499.
Location/Qualifiers
                                                                                                                                      tccagtgtaatcagtgcggggatcttttactcagaaaggtaacctcctccgtcatatta 866
                                                                                                                                                                                                                                                                                  489 CCCAGTGTAATCAGTGC-GGGCATCTTTTACTCAGAAAGGTAACCTCCTCCGTCATTA 431
                                                                                                               Gaps
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Unpublished (1996)
On Jan 17, 1998 this sequence version replaced gi:2044537
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                             Indels
                                                                                Length
                                                                             Score 204; DB 40;
Pred. No. 2.9e-39;
0; Mismatches 15;
Bonaldo."
171 t
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1281978"
/clone=lib="Soares 2NbMT"
 and M.Fatima
2 c 152 g
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                                                                             10.3%;
93.1%;
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Matches 257; Conservative
    Soares
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AA866707
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AA866707/C
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Those—"Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5] read of property and the strand cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Falma Bonaldo."
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 217)
NCI-CGAP http://www.ncbl.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1556 cgc-caacatctctaccagcaaagccacgtggtcctcccccaggcccgcaatgggatgcc 1614
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62.2%; Pred. No. 5.1e-29;
tive 0; Mismatches 172;
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/strain="C57BL/6J"
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AA920812.1 GI:3067591
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//dev_stage="4 weeks"
//dev_stage="4"
                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 332)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martlin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 302.
Location/Qualifiers
1. .332
Gorganism="Mus musculus"
/strain="C57BL/6J"
/db_xref="txon:10090"
/map="1; 763Ell: 5; 5q13.2-5q14.1; Chromosome 7; 21q"
/clone="IMAGE:1264352"
/clone="IMAGE:1264352"
/clone=lib="Soares 2NbMT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGTGTGTACCCCATAGCACTTACNTCGGCCGATTACTCCAATGGGGCCCCGCAGGAGA 212
                        AA867722 332 bp mRNA EST 16-MAR-1998 vxl3e05.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1264352 similar to TR:008900 008900 AIOLOS ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2150693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Washington University School of MedicineP
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89.8%; Pred. No. 4.9e-55;
tive 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                                                                                                                                       AA867722.1 GI:2963167
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                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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JOURNAL
                                                                                                                            ACCESSION
                                                                                                                                                                                           VERSION
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 609)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
1506 ccaataacagtgcccaggactccacagacaccgacagcaaccacgaggatcgccaacatc 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA920812 609 bp mRNA EST 20-APR-1998 vx86f12.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1282127 similar to TR:008900 008900 AIOLOS ;, mRNA sequence.
                                                                                                                            The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1407236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 423. Location/Qualiflers
                                                                                                                                                                                                                                                                                               1626 aggtccttcgctctttgaactcctcaagcccc 1659-
                                                                                                                                                                                                                                                                                                                                             34 AGGICCCICGCICTIGAACICCCCAGCCCCCIC 1
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    .609
    /organism="Mus musculus"

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/clone="IMAGE:1282127"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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86
                                   TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 gaaggggaaggtgatggatgtgtttcgatgtgaccactgccacgtcctcttcctagattat 1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:458077
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 485.
Location/Qualifiers
1.517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 401)
Marra.M. Hillier.L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone=lib="Soares mouse 3NbMs"
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                                                                                                                                                                                                                                                                                                                                                                                                  14.1%; Score 279; DB 31;
100.0%; Pred. No. 2.3e-57;
tive 0; Mismatches 0;
mouseest@watson.wustl.edu
                                                                                                                                                                            /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
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AI644775.1 GI:4723250
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Matches 279; Conservative
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/issue_rype="Spleen"
/dev_stage="4 weeks"
/dev_stage="4 weeks"
/lab_host="Dato#" weeks"
/lab_host="Dato#" weeks"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note="Vector: pT73D-Pac (Pharmacia) with a Not I: Site_2: Eco RI: 1st strand cDNA
was primed with a Not I: oligo(dT) primer [5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R.
The Wash Urol Mouse EST Project 1999
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:458077
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Fax: 314 286 1800
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                                                                                                                                                                                                                                                                        On May 7, 1998 this sequence version replaced gi:3121606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/WashU-NCI Mouse EST Project 1999
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: -40RP from Glbco
High quality sequence stop: 358.
Location/Qualifiers
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Fax: 314 286 1810
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                                                                                                          Similarity
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                                                                                                                       Matches 475;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodeniia; Sciurognathi; Muridae; Murinae; Mus. 1 (2008) 1 to 480)
Maria, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Marta, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R., The WashU-NcI Mouse EST Project 1999
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced 91:3188293.
                                                                                                                                                                                                                                                                    AISO9603 480 bp mRNA EST 12-MAR-1999 vx13e05.yl Soares 2NbMT Mus musculus cDNA clone IMAGE:1264352 5' similar to 9b:L03547 Mouse Ikaros DNA binding protein (MOUSE);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL ; contact the IMAGE_Consortium (info@image.llnl.gov) for further information.
                                                                                                       826
                                               99/
                                                                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Frax: 314 286 1810
Email: mouseest@watson.wustl.edu
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/61"
/db_xref="taxon:10000"
/clone="IMAGE:1264352"
/clone=lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: -40RP from Gibco
High quality sequence stop: 467.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                gcatctttactcagaaaggt 847
                                                                                                                                                                                 94408508
AI509603.1 GI:4408508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AI509603
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:666904
                                                                                                                                                                                                                                                                                                                                                                             EST.
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                                                                                                                                                                                                                                         RESULT 4
AI509603/c
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JOURNAL
COMMENT
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AUTHORS
            301
                                                                                                                                                                827
                                                                                                                                                                                                                                                                                                                              ACCESSION
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KEYWORDS
SOURCE
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4

FEATURES

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AA290536 517 bp mRNA EST 14-APR-1997 vb16d03.rl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:749093 5' similar to gb:L03547 Mouse IKaros DNA binding protein (MOUSE);, AA290536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 517)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 ctctgagatggtcccagtcatcagcagtgtgtaccccatagcacttactcgggccgatat 1422 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 
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     by Bento
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1243 gtacgagaaggagaacgagatgatgcagacccggatgatggaccaagccatcaataacgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 GCCTTCTGAACGAGGTCTGTCCCCCAATAACAGTGCCCAGGACTCCACAGACACCGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393523.
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          was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                          Score 472; DB 47;
Pred. No. 7.2e-104;
); Mismatches 5;
rounds of normalization, and
Soares and M.Fatima Bonaldo."
112 c 159 g 121 t
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                                                                                                                                                                                                                                                                                                          23.8%;
99.0%;
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3/]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p1713 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

118 c 143 g 81 t l others
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                         This clone was previously sequenced on the 5' end only, this new data is from the 3' end data is from the 3' end bossible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found High quality sequence stop: 381.
                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:666904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 gctgcagcccgcgcgcgcggcgacatggaagatatacaaccgactgtggagctgaaa 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gaatacagcgactatgaaagcattaagctggagagacacgtgccctatgacaacagcaga 706
                                                                                                                             Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1264352"
/clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .501
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Best Local S
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       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                     458 INCIGCAACTACGCATGCCAAAGGAGAAGGATGCGCTCACGGGACACCTTTAGGACACATTC 399
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                                                                                                                                                                                                                                                                             GAAGCGGCACTGCTTCGATGCCAACTACAATCCCGGCTACATGTACGAGAAGGAACGA
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                                                                                                                                                                                                      DB 39; Length 577;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 501)
                                                                                                                                                                                                                               Indels
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Pred. No. 1.7e-111;
0; Mismatches 26;
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                                                                                                                                                                                                     Query Match 25.4%;
Best Local Similarity 95.0%;
Matches 550; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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Gaps

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180 586 240 646

991 420

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Mus musculus

Bukaryota, Martazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 577)

Marta, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                     AA863970 577 bp mRNA EST 11-MAR-1998 vx87d08.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1282191 similar to TR:008900 008900 AIOLOS ;, mRNA sequence.
                                                                          atgaagccggagcccatgggagatgcagaagagagtgaaatgccttacagctatgcaaga
                                                                                                                                                                                                                                                                                                gcatcttttactcagaaaggtaacctcctccgtcatattaaactgcacacgggggaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU HHMI Mouse EST Project
Unpublished (1996)
On Jun 27, 1996 this sequence version replaced gi:1184736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity on wrong strand
Seg primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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AA863970/c
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AUTHORS
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JOURNAL
COMMENT
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                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 546)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                  MGI:665884
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
data is from the 3' end
data is from the 3' end
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Possible reversed clone: polyT not found
High quality sequence stop: 460.
Location/Qualifiers
1. .546
                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 gctgcagcccgcgcggcccgcggcgacatggaagatatacaaccgactgtggagctgaaa 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cccaaacctcatgagatagaaaacgtggacagtagaagaccccagccaatgaagacgaa 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 5, 1998 this sequence version replaced gi:3189635.
                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 543.4; DB 48; Length 546;
Pred. No. 4.8e-121;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                       Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.48;
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house mouse.
Mus musculus
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                                                                                                                                                                                TITLE
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                                                                        REFERENCE
                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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Page 1

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

November 6, 1999, 08:08:27 ; Search time 437.25 Seconds (without alignments) 8950.272 Million cell updates/sec ron on:

US-09-019-348-1 1984 1 cacgagcgcacaccgctcgg......gaactcaaacccacctcgag 1984 IDENTITY_NUC Title: Perfect score: Sequence: Scoring table:

2546578 seqs, 986266752 residues EST:* Database : Searched:

em_est1::
em_est2::
em_est4::
em_est4::
em_est7::
em_est8::
em_est8::

em_est10:* em_est11:* em_est12:*

em_est22:*
em_est23:*
em_est24:*
em_est25:*
em_est25:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ription	AI549961 vx02e08.x	863970 vx87d08.	500402 VX13605.	90536 vb16d03	644775 vb16d03.	867722 vx13e05.	20812 vx86f12.	56707 vx85a10.	10940 ov53b04.	25349 m106e03.	28749 vv49e05.	08413 oa43h06.	108 ys90h12.rl	54246 vv49e05.	19538 mposaus.	407 VD69C09	18430 EST19119	169 zb25b08.rl	27561 m106e03	11308 UI-R-C3-	4	501 35a3 Huma	18952 uk33c0	39228 vc93q04	189 HSAAADRRE	79640 EST2233	304 ye	256 YG24 NU5.r	524 YG4/AUL.II	03426 mg48h01.	27841 zw49e10	1439 vf81f04.	14904 mr74a08.	14289 Homo sap	395 ys14h07.r	551 yl75b08.r	55712 aa22e04.	99468 v185h1	124541 am58e03.	A920944 vy15d06.	944 ym33f11.
ΩI	AI549961	36397	04000	29053	54477	36772	92081	36670	1094	2534	2874	3841	80	5424	1400	AA400326	34843	9169)27	51130	W28371	1007	AT648952	28922	1189	179	30	200	10653	0342	127	45143	90	M0091	σ	5551	45571	499	AI124541	92094	94
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ALIGNMENTS

em_est13:...
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A1549961 546 bp mRNA EST 23-MAR-1999 vx02e08.x1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1263302 3' similar to TR:008900 008900 AIOLOS ;, mRNA sequence. AI549961 44482324 AI549961.1 GI:4482324 RESULT 1 AI549961 LOCUS DEFINITION ACCESSION NID VERSION

gb_est30:*
gb_est31:*
gb_est32:*
em_est20:*

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9.6%; Score 191.2; DB 5;
Pest Local Similarity 61.6%; Pred. No. 4.3e-42;
Matches 405; Conservative 0; Mismatches 223;
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AscII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
FILING DATE:
                                                                                                                                                                                                                                                   PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-UULY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY AGENT INFORMATION:
E: LAHIVE & COCKFIELD
60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MGP-027PC TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400 TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Myers, Paul L. REGISTRATION NUMBER: 35,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1296 base pairs
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EDNESS: single
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ADDRESSEE: LAI
STREET: 60 ST
CITY: BOSTON
STATE: MASSACI
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PCT-US95-09345-3
                                                                    COUNTRY:
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Search completed: November 6, 1999, 06:57:37 Job time: 138 sec

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                          1365 ctgagatggtcccagtcatcagcagtgtgtaccccatagcacttactcgggccgatatgc 1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
UNMBER OF SEQUENCES: 164
CURRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1993
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08465590 Patent No. 5824770 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: BOSTON
STATE: MASSACHUCETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-465-590-7
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Sequence 1.NFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                            9.6%; Score 191.2; DB 3
61.6%; Pred. No. 4.1e-42;
tive 0; Mismatches 223
                        MPG-006C2DV
REGISTRATION NUMBER: 35,695
REPERBENG-FOOKET NUMBER: MC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      LENGIH: 1128 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                        1..1128
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                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-465-590-7
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Matches 405;
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                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 4.3e-42;
0; Mismatches 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              3: LAHIVE & COCKFIELD
60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
                                                                                                                                                                                       RESULT 13
US-08-465-590-4
; Sequence 4, Application US/08465590
; Patent No. S24770
                                                                                                      1857 ctcacatcgccagaggagagca 1878
                                                                                                                             1133 CCCATATCACGCGGGGGAGCA 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Myers, Paul L. REGISTRATION NUMBER: 35,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEO ID NO: 4: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 61.6
Matches 405; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                STATE: MASSACHUCETTS
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STRANDEDNESS:
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US-08-465-590-4
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                                                                                                                                                        54;
                                                                                                                      Length 1170;
                                                                                                                                                       Indels
                                                                                                                                      Pred. No. 7e-54;
0; Mismatches 393;
                                                                                                                      DB 5;
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                                                                                                                      Score 235.2;
                                                                                                                   Query Match 11.9%;
Best Local Similarity 57.1%;
includes 595; Conservative
MOLECULE TYPE: CDNA FEATURE:
                                                  1..1170
                                   CDS
                                : NAME/KEY:
; LOCATION:
PCT-US95-09345-5
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                                 1566 tctaccagcaaagccacgtggtcctccccaggcccgcaatgggatgcctcttctgaagg 1625
                                                                893 AGGAGCAGCGCCCTACGAGGTGCTGAGGGCGGCCTCAGAGAACTCGCAGGATGCCTTCC 952
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GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTON: IRAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-UULY-94
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
FRICK APPLICATION NUMBER: US 08/121,438
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1857 ctcacatcgccagaggagagca 1878
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REGISTRATION NUMBER: 35,69:
REFERENCE/DOCKET NUMBER: MC
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617)227-7400
TELEPRAX: (617)227-7400
TELEPRAX: (617)227-5941
INFORMATION FOR SED ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 1170 Dasse pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE STRE.
STATE: MASSACHUSETTS
COUNTRY: USA
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PCT-US95-09345-5
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Pred. No. 7e-54;
0; Mismatches 393; Indels 54;
                                                                     NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)227-7400
TELEFAX: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER: US 07/946,233 FILING DATE: 14-SEP-1992 ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 57.1%;
Matches 595; Conservative
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; LOCATION: 1..1
US-08-465-590-6
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400 AACGCCATCAACTACCTGGGGGCCGAGTCCCTGCGCCCGCTGGTGCAGACGCCCCCGG-- 458

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APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                              1358 occacetetgagatggteecagteateageagtgtgtaceeat-
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,590

FILING DATE: 05-JUN-1995

PRIOR APPLICATION NUMBER: US/08/238,212

FILING DATE: 02-MAY-1994

PRIOR APPLICATION NUMBER: US/08/121,438

FILING DATE: 14-SEP-1993

PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: LAHIVE & COCKFIELD .
60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-465-590-6; Sequence 6, Application US/08465590; Patent No. 5824770
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                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09345
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: MGP-027PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-5EP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-JULY-94
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/946,233 FILING DATE: 14-SEP-1992 ATTORNEY/AGENT INFORMATION:
                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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PCT-US95-09345-7
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Best Local Simi
Matches 602;
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CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
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COMPUTER READABLE FORM:
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Sequence 8, Application US/08465590
Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1004;
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Pred. No. 4.1e-63;
0; Mismatches 369;
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ACCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/21,438
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                             E: LAHIVE & COCKFIELD
60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFRENCE/DOCKET NUMBER: MPG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
13.6%;
Best Local Similarity 58.9%;
Matches 602; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                STREET: 60 STATE STRI
CITY: BOSTON
STATE: MASSACHUCETTS
COUNTRY: USA
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Best Local Similarity
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US-08-465-590-8
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1118 agtgagagatetegteetggacagattageaagcaatgtggetaagegaaaaageteg 1177
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TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
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PCT-US95-09345-7; Sequence 7, Application PC/TUS9509345; GENERAL INFORMATION:
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                                                                                                                                                                      APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 346.4; DB 5;
Pred. No. 1.5e-83;
0; Mismatches 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MGP-027PC
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US95/09345
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-UULY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
                                                                                                                                             Sequence 1, Application PC/TUS9509345 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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62.0%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.09
Matches 715; Conservative
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
                                                   1886 atgttgaagtgage 1899
                                                                            1507 CACCTGAGCTAAAC 1520
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EDNESS: single
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CITY: BOSTON
STATE: MASSACH
                                                                                                                                                                                                                                                                                    USA
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LOCATION:
PCT-US95-09345-1
                                                                                                                     RESULT 8
PCT-US95-09345-1
                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                 502 GCCTGCCGCCGGAGGGACGCCCTCACCGGCCACCTGAGGACGCACTCCGTTGGTAAGCCT
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                                                                   1090 TCTGTGTCATCGGAGGGGGAGAGGCCTCCCGAGCAACAGCTGCCAAGACTCCACAGATACA 1149
                                                                                           gacagcaaccacgagg---atcgccaacatctctaccagcaaagccacgtggtcctcccc 1594
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                  1030 CGGTCCAACCATTCAGCACAGACGCCGTGGATAACTTGCTGCTGCTGTCCAAGGCCAAG
                                             atcttgccttctgaacgaggtctgtcccccaataacagtgcccaggactccacagacacc
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
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Pred. No. 1.5e-83;
0; Mismatches 376;
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APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELECOMNUNCATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9308743
GENERAL INFORMATION:
APPLICANT:
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62.0%;
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LENGTH: 1788 base pairs
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Hest Local Similarity 62.0
Matches 715; Conservative
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LOCATION:

LOCATION:
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gaaggaggtccctcgctcttttgaactcctcaagcccctcccatctgcctgagggactc 1680
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                                                                                           1200 ATTGGTGCAGACACCCCCGGGT---AGCTCCGAGGTGCTGCCAGTCATCTA
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Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTON: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-UN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
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60 STATE STREET, Suite 510
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: MASSACHUCETTS
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STREET: 60
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         FILING DATE: 14-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-5EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECHONE: (617)227-7400:
                                                                                                                                                       TELEFAX: (617)227-5941
INPORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.0
Matches 715; Conservative
                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    223..1515
APPLICATION NUMBER:
                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                      ; NAME/KEY;
; LOCATION:
US-08-465-590-2
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 cgatgccaactacaatcccggctacatgtacgagaaggagaacgagatgatgcagacccg 1275
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
RPLICATION NUMBER: PCT/US95/09345
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application PC/TUS9509345
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IRAROS TRANSGENIC
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALUNKESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: ACT.
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PCT-US95-09345-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 379.6; DB 5; Length:
Pred. No. 2.1e-92;
0; Mismatches 414; Indels
                         PADLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REERCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           TELEFAX: (61)727-5941
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 61.8%;
Matches 771; Conservative
                                                                                                                                                                                                                                                                                                                                  LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
29-JULY-94
            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 223..1776
PCT-US95-09345-4
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
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1108 ----CTCAAGGAGGAGCACCGCGCCTACGACTGCTGCGCGCCGCCCTCCGAGAACTCGCA 1163
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                 1441 ggagatggaaaagaaacggatcctcctgccagagaagatcttgccttctgaacgaggtct
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1153 caatgiggctaagcgaaaaagctcgatgcctcagaaattcatcggtgagaagcggcactg
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Patent No. 5824770
FENERAL INFORMATION:
ADDITIONAL INFORMATION:
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
SYREAT: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUCETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1855 ctctcacatcgccagaggagagcacag 1881
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.1%; Score 379.6; DB 3; Best Local Similarity 61.8%; Pred. No. 2.1e-92; Matches 771; Conservative 0; Mismatches 414;
                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212.
FILING DATE: 02-MAX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-5EP-1992
ATTORNEY/AGENT INFORMATION:
SOFTWARE: AscII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-UUN-1995
                                                                                                                                                                                                                                            NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2049 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
223..1776
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-465-590-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 411.8; DB 5;
Pred. No. 4.2e-101;
0; Mismatches 387;
                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,300
FILING DATE: 29-UULY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-589-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,438
FILING DATE: US 08/231,438
APPLICATION NUMBER: US 07/946,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MGP-027PC
COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCIT /*****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1386 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.8%;
                                          CURRENT APPLICATION (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/U
PRIOR APPLICATION NUMBER: PCT/U
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 777; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
1..1386
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; LOCATION:
PCT-US95-09345-2
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                                                                                                                                                                                                582 GGCAGAAGACCTGTGCAAGATAGGATCAGAGATCTTCTCGTGCTGGACAGACTAGCAAG 641
                                                                                                                                                   642 TAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGGGCCTGTC 701
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GENERAL INFORMATION:
AFFLICANT: Georgopoulos, Katia A.
ITILE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
UNMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: LAHIVE & COCKFIELD
60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1344 Gregeacaraaceceaegegeaecec 1370
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COSTREET: 60 STATE STREE CITY: BOSTON STATE: MASSACHUSETTS
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PCT-US95-09345-2
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                                                       864 TAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGGGCCTGTC
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TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
1060 ccctgacct--gggggacgctgcaagtgtggaggcaagacacatcaaagc-
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-465-590-3; Sequence 3, Application US/08465590; Patent No. 5824770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GEOTGO
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Pred. No. 4.2e-101;
0; Mismatches 387;
                                                                                                                                                                                                                                                                                                                                                               NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227,7400
                                                                                                                                                                    FILING DATE: 05-UN-1955
PRIOR APPLICATION DATE: 05-UN-1955
APPLIANG DATE: 05-UNA-1994
FILING DATE: 07-WAX-1994
PRIOR APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1993
ATTORNEY, AGENT INFORMATION:
                                                                                                                SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-UN-1995
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.8%;
63.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)227-5941
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1386 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 63.3
Matches 777; Conservative
MASSACHUCETIS
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                   USA
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MOLECULE TYPE:
                                ZIP: 02109
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; LOCATION:
US-08-465-590-3
 STATE: N
COUNTRY:
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us-09-019-348-1.rni

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

November 6, 1999, 06:55:19; Search time 44.29 Seconds (without alignments) 4660.693 Million cell updates/sec Run on:

US-09-019-348-1 1984 1 cacgagcgcacaccgctcgg......gaactcaaacccacctcgag 1984 ritle: Derfect score: Sequence:

IDENTITY_NUC Scoring table: searched:

. 50000000

192659 seqs, 52021692 residues

issued_Patents_NA:*

/ cgn2_6/ptodata/l/ina/5A_COMB.seq:*
// cgn2_6/ptodata/l/ina/5B_COMB.seq:*
// cgn2_6/ptodata/l/ina/5C_COMB.seq:*
// cgn2_6/ptodata/l/ina/5C_COMB.seq:*
// cgn2_6/ptodata/l/ina/PCTUS9_COMB.seq:*
// cgn2_6/ptodata/l/ina/pctus9_COMB.seq:*
// cgn2_6/ptodata/l/ina/packfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ription	Sequence 3, Appli Sequence 2, Appli Sequence 5, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 17, Appli Sequence 11, Appli
	PCT-US93-08743-3 US-08-465-590-3 US-08-465-590-5 PCT-US95-09345-2 PCT-US95-09345-2 PCT-US95-09345-7 US-08-465-590-8 PCT-US95-09345-7 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-465-590-4 US-08-933-750C-65 US-08-933-750C-65 US-08-933-750C-65 US-08-933-750C-63 US-08-933-750C-63 US-08-933-750C-63 US-08-933-750C-63 US-08-933-750C-63 US-08-933-750C-63 US-08-933-750C-63 US-08-933-750C-63 US-08-93-750C-63 US-08-93-750C-63 US-08-93-750C-63 US-08-144-95-7 US-08-040-548-15 US-08-040-548-11 US-08-040-548-11 US-08-040-548-11 US-08-040-548-11
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857-1 590A-39 3940-1 3940-2 3940-3 3940-4 3940-6	STN	PATHWAY RI	.8; DB 5 1.3e-101 ches 397	acgtgtgcggg ATATCTGTGG	cggcgaacg TGGAGAACG	cctccgtca GCTCCGGCA	cgcatgcca cGCCTGCCG	gtacaagtg' TCACAAAIG
US-08-616-85 US-08-398-59 PCT-US96-039 PCT-US96-039 PCT-US96-039 PCT-US96-039	ALIGNMENT	308743 A T CELL MS-DOS MS-DOS 6,233 N:	Score 413 Pred. No. 0; Mismat	tgaactgcg TAAAGTGTG	caacytcttgatgyttcataagcgaagccataccggcgaacgcccgttccagtgtaatca 	gtgcgggcatctttactcagaaaggtaacctcctccgtcatattaaactgcacacggg 	gaaaaaccttttaagtgtcacctctgcaactacgcatgccaaaggagagatgcg 	gggacaccttaggacacattctgtggagaagccgtacaagtgtgagttctgcgggaagaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severally immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders Disclosure; page 71-73; 107pp; English.

A cDNA clone (716065) coding for an Ikaros protein (R92020) has been identified. Transgenic animals, pref. mice, having a mutated Ikaros transgene, esp. a mutation that alters the DNA binding domain of the Ikaros protein, are used as models to determine the effects of treatments for immune or nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1058 aaccctgacctgggggacgctgcaagtgtggaggcaagacacatcaaagccgagatggga
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                                                                                                                                                                                                       immunocomprised; immune system disorder; nervous system disorder; animun model; ss. Not specified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 T;
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                                                         standard; cDNA; 1004 BP
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29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
Georgopoulos K:
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P-PSDB; R92020.
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Matches 602;
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T16065;
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                                                                                                                                 748 TACGACCTGCTGCGCGCCCTCCGAGAACTCGCAGGACGCGCTCCGCGTGGTCAGCACC
                                                                           577 TCCAAGGCCAAGTTGGTGCCCTCGGAGGGGGGAGGCGTCCCCGAGCAACAGCTGCCAAGAC
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Search completed: November 6, 1999, 02:38:40 Job time: 18371 sec

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Por System or corpus striatum

Por System or corpus striatum

Por Discloaure; Column 51-56; Illpp; English.

Co the following properties; (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFNB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFNB element or an Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikaros isoform to any of a delta A element, an NFNB element or an Ikaros binding oligonucleotide consensus sequence; (d) it competitively inhibits Ikaros binding to Ikaros responsive elements; or (e) it inhibits protein-protein interactions of transcriptional complexes formed with naturally occurring Ikaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements and/or Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-responsive elements and/or inhibit protein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system of allohibate protein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system of allohibate protein protein protein protein at AlDS, or corpus striatum disorders, e.g.
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14-JAN-1999 (first entry)
Murine Ikaros encoding cDNA mIk-2.
CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
differentiation marker; immune system; corpus striatum; AIDS;
Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctccgtcatattaaactgcacacgggggaaaaaccttttaagtgtcacctctgcaactac 913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ikaros poly:peptide(s) - useful for treating disorders of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders, e.g. leukaemia or AlDS, or curpus series. Alzheimer's disease. The present sequence encodes a specifically claimed mouse Ikaros protein.

Sequence 1788 BP; 437 A; 486 C; 495 G; 370 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.5%; Score 346.4; DB 1; Length 1788; 62.0%; Pred. No. 1.4e-77;
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                                                                                                                                                                                                                                                                                          Location/Qualifiers
223. .1518
/*tag= //
/product "mik-2"
/transl_except= (pos:385. .387,aa:Gln)
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                                                                                                                                                             V66968 standard; cDNA; 1788 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1992; US-946233.
14-SEP-1993; US-121438.
05-JUN-1995; US-465590.
(GEHO ) GEN HOSPITAL CORP.
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15; Conservative
                                              1886 atgttgaagtgägc 1899
                                                                              1507 CACCTGAGCTAAAC 1520
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WPI; 98-582621/49.
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05-JUN-1995;
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Matches 715;
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gcatgccaaaggagagatgcgctcacgggacaccttaggacacattctgtggagaagccg
                  gaacgctgccgagcttttcttcagaaccctgacctgggggacg.....ctgcaagtgtg
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CONA clones (T16059 and T16061-64) encode different isoforms, mik-2, mik-3, mik-1, mik-4 and mik-5 (R92014 and R92016-19, respectively), of the mouse Ikaros protein, a master regulator of hematopoietic differentiation. They were isolated from a mature T-cell line E-14 cDNA library. The isoforms arise by differential splicing of the Ikaros genomic locus. All include exons E1/2 and E7, but have different candinals, pref. mice, having a mutated Ikaros transgene, esp.

Transgenic animals, pref. mice, having a mutated Ikaros transgene, esp.

Transgenic animals, pref. bNA bluding domain of the Ikaros protein, an experience a mutation that alters the DNA bluding domain of the ikaros protein, and a mutation is madels to determine the effects of treatments for immune
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                                                                                                                                                           gatgigittegatgigaceactgecacgicetetteetagattatgigatgiteaecaie 1774
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---atcgccaacatctctaccagcaaagccacgtggtcctcccc 1594
                                                                                                                                                                                                            caggocogoaatgggatgoctcttctgaaggaggtcoctcgctctttgaactcctcaag
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disorder;
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                                                                           CATGCACGCAATGGGCTGGCTCTC---AAGGAGGAGCAGCGCGCCCTACGAGGTGCTGAGG
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08-MAY-1996 (first entry)
Murine Ikaros CDNA mIK-2.
IKaros; transgene; transgenic animal; transgenic mouse;
Immunocomprised; immune system disorder; nervous system
animal model; ss.
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/transl_except= pos:385. .388:_aa:Gln
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Pred. No. 1.4e-77;.
0; Mismatches 376;
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233. .1518
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quence 1788 BP; 437 A;
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62.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                T16059 standard; cDNA; 1788
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Georgopoulos K;
WPI; 96-129389/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 17.5
Best Local Similarity 62.0
Matches 715; Conservative
                                                                                                                                                                                                                                                                                                                                                 CACCTGAGCTAAAC 1520
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15-FEB-1996.
28-JUL-1995; U09345.
29-JUL-1994; US-28330
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ggcgaacgcccgttccagtgtaatcagtgcggggcatctttactcagaaaggtaacctc
                                                                                  ctccgtcatattaaactgcacacgggggaaaaaccttttaagtgtcacctctgcaactac
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                                                                                                                                                                                                                                                                          622 GAGCGATGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCGTGTGCCCAGTCATTAAG
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(GEHO ) GEN HOSPITAL CORP.
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CTTGTCCTGGACAGGCTGGCAAGCAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAA
                                TTTCTTGGAGACAAGTGCCTGTCAGACATGCCCTATGACAGTGCCAACTATGAGAAGGAG
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/product- Ikaros protein.
385. .387
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Ikaros; zinc finger; protein; immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                Treell pathway regulatory gene, Ikaros - encodes family of unique zinc finger proteins, useful for treating immune system disorders claim 13: Page 41-43; 112pp; English.

The Ikaros gene encodes a zinc finger protein which can be used in therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is risk for an immune disorder. It is of particular use in treating disorder of the corpus striatum.

Sequence 1788 BP; 437 A; 486 C; 495 G; 370 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1788,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 346.4; DB 1; Length
Pred. No. 1.4e-77;
0; Mismatches 376; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.0%;
Matches 715; Conservative
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Georgopoulos K;
WPI; 94-118387/14.
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Persons; W70963.

New nucleic acid encoding Ikaros protein involved in early new nucleic acid encoding Ikaros protein in several isoforms, and related products, used to treat e.g. immune diseases or cancer and related products, used to treat e.g. immune diseases or cancer and related products, used to treat e.g. immune diseases or cancer and claim 7: Page 68-70: 158pp; English.

This is the nucleotide of mouse Ikaros cDNA (isoform mIk-2) that codes for a 41-amino acid zinc finger protein (see W70963) that is involved in the early differentiation of lymphocytes. A CDNA library constructed from the mature murine T cell line E14 was screened with a multimerised oilgonucleotide (see W4289) derived contained the 1788 bp sequences that bind and mediate enhancer function. An isolated clone was designated likaros and contained the 1788 bp sequence. A 300 bp 3-terminal segment of this was used to identify 4 other Ikaros isoforms (see W42807-10). Different isoforms mik-2 lacks scorns is located at the proximal arm of murine chromosome 11. Ikaros gene is located at the proximal arm of murine chromosome 11. Ikaros gene is located at the proximal arm of murine chromosome 11. Ikaros gene is located at the proximal arm of murine chromosome 11. Ikaros proteins are suggested to play a role as a genetic switch regulating entry into the T cell lineage. The murine and human (see W42806, w12811 and w12840) ikaros sequences are very similar. The invention provides Raros nucleic acids, vectors and host cells expressing Ikaros proteins. These are used to treat T and B cell diseases (e.g. immune deficiencies caused by drugs, radiation or cancers), to control expression of heterologous creat nervous system diseases (e.g. immune deficiencies caused by drugs, radiation are annexed to inhibit interaction or differentiation or cancers), to control expression of the same effect can be achieved with Ikaros specially sequences. The same effect can be achieved with Ikaros special sequences of the same effect can be achieved with Ikaros special 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 348; DB 1; Length 1788;
Pred. No. 5.5e-78;
0; Mismatches 375; Indels 6
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                           (GEHO ) GEN HOSPITAL CORP
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                                                                            WPI; 98-378292
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Mouse Ikaros isoform mIk-2 cDNA.
HAROS: mIK-2; transcription factor; mouse; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; ss.
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Mouse Ikaros isoform mik-1 cDNA.
Ikaros: mik-1; transcription factor; mouse; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; ss.
Mus sp.
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Claim 7; Page 75-77; 158pp; English.

This is the nucleotide of mouse Ikaros CDNA (isoform mIk-1) that codes for a 518-maino acid zinc finger protein (see W10966) that is involved in the early differentiation of Iymphocytes. mIk-1 CDNA was isolated from a mature murine T cell line E14 library using a 100 bp fragment from the 3' end of mIk-2 CDNA (see V42805) as probe. 5 Different isoforms of mouse Ikaros (see V42805) as plicing of Ikaros gene transcripts. Isoform mIk-1 contains all 7 exons. It is abundantly expressed in the early foetal liver, the maturing thymus and the postnatal spleen. The Ikaros gene is coated at the proximal arm of murine chromosome 11. Ikaros proteins are suggested to play a role as a genetic switch regulating entry into the T cell lineage. The murine and human care usual to proteins are suggested to play a role as a genetic switch regulating entry into the T cell lineage. The murine and human care lives and v42806, v4281 and v42840 likaros sequences are very similar. The invention provides Ikaros nucleic acids, vectors and host cells expressing Ikaros proteins. These are used to treat T and B cell diseases (e.g. limmune deficiencies caused by drugs, radiation or cancers), to control expression of heterologous genes placed under control of an Ikaros-responsive element, to treat nervous system amplification or differentiation, especially in haematopoietic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences. The same effect can be achieved with Ikaros-binding oligonucleotides. Examining the expression of the Ikaros gene, or its allelic structure, can be sequenced. States of acquiring the above diseases.
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                                                                                                                                               New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, related products, used to treat e.g. immune diseases or cancer to control cell differentiation
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Pred. No. 7e-86;
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WPI; 98-378292/33.
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CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
differentiation marker; immune system; corpus striatum; AIDS;
Alzheimer's disease; ss.
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The present invention describes a purified peptide having
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                                                                                               ccccatagcacttactcgggccgatatgccaatgggggcc----
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ID V66971 standard; CDNA; 2049
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14-SEP-1992; US-946233.
14-SEP-1993; US-121438.
05-JUN-1995; US-465590.
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WPI; 98-582621/49.
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of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFKB element or an Ikazos binding oilgonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFKB element or an Ikazos binding oilgonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikazos sioform to any of a delta A element, an NFKB element or an Ikazos binding oilgonucleotide consensus sequence; (d) it competitively inhibits Ikazos binding to Ikazos responsive elements; or competitively inhibits protein interactions of transcriptional complexes formed with naturally occurring Ikazos isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements and/or Ikazos-binding oilgonucleotides, competitively inhibit binding of naturally occurring Ikazos binding of competitively inhibit Ikazos binding of Ikazos-binding oilgonucleotides, competitively inhibit Ikazos binding of Ikazos-responsive elements and/or competitively inhibit Ikazos binding of Ikazos-responsive elements and/or competitively inhibit Ikazos binding of transcriptional complexes with naturally occurring Ikazos binding of transcriptional complexes with caturally occurring Ikazos binding of transcriptional complexes with caturally occurring Ikazos isoforms, can be used to treat immune system disorders, e.g. leakaemia or AIDS, or corpus striatum disorders, e.g. classaes. The present sequence encodes a specifically calamed mouse Ikazos protein.
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Pred. No. 7e-86;
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Best Local Similarity 61.8%;
Matches 771; Conservative
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                                 CCCGCTGGTGCAGACGCCCCCGG---GCGGTTCCGAGGTGGTCCCGGTCATCAGCCCGAT
                                                   gtaccccata------gcacttactcgggccgatatgccaatgggggcccgca
                                                                                                                                                                                                                                 Haros; transgene; transgenic animal; transgenic mouse; mIk-1; immunocomprised; immune system disorder; nervous system disorder; animal model; ss.
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223. .1779
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                                                                                                                                                                                                                                                                                Disclosure: Page 65-67; 102pp; English.

CDNA clones (T16059 and T16061-64) encode different isoforms, mix-2, mix-3, mix-1, mix-4 and mix-5 (R92014 and R92016-19), respectively), of the mouse Ikaros protein, a master regulator of hematopoietic differentiation. They were isolated from a mature 7-cell line E-14 CDNA library. The isoforms arise by differential Splicing of the Ikaros genomic locus. All include exons E1/2 and E7, but have different combinations of exons E3-E6 encoding a fine figured domain. Transgenic animals, pref. mice, having a mutated Ikaros transgene, esp. a mutation that alters the DNA binding domain of the Ikaros protein, are used as models to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gggacaccttaggacacattctgtggagaagccgtacaagtgtgagttctgcggaagaag
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                                                                                                                                                                                                Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determine the effects of treatments for immune or nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
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Pred. No. 7e-86;
0; Mismatches 414; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.1%;
61.8%;
15-FEB-1996.
28-JUL-1995; U09345.
29-JUL-1994; US-283300.
(GEHO ) GEN HOSPITAL CORP.
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Matches 771; Conservative
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                                                                                                                 Georgopoulos K;
WPI; 96-129389/13.
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differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and to control cell differentiation

Claim 1: Page 127-129: 158pp: English.

This is the nucleotide of human Ikaros cDNA (isoform hIk-1) that codes for a 516-amino acid zinc finger protein (see W10971) that is involved in the early differentiation of lymphocytes. It was isolated from a Jurkat T cell line library using mouse ikaros exon convolved in the early differentiation of lymphocytes. It was isolated from a Jurkat T cell line library using mouse ikaros exon chromosome 7. The human and murine ikaros sequences (see V42805-11 and V42840) are highly conserved. Differential splicing of Ikaros and V42840 provides Ikaros nucleic acids, vectors and host cells expressing Ikaros proteins. These are used to treat T and B cell diseases (e.g. immune deficiencies caused by drugs, radiation or ancers), to control expression of heterologous genes placed under control of an Ikaros responsive element, to treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, amplification or differentiation, especially in haematopoletic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences. The same effect can be achieved with Ikaros-binding oligonucleotides. Examining the expression of the Ikaros gene, or its allelic structure, can be used to assess risk of acquiring the above diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccggatgatggaccaagccatcaataacgccatcagctatctaggggctgaagccttccg 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cttcgatgccaactacaatcccggctacatgtacgagaaggagaacgagatgatgcagac 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cagcagaccaaccagtgggaagatgaactgcgacgtgtgcgggttatcctgcattagctt 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 CATTCGACTTCCTAACGGAAAACTAAAGTGTGATATCTGTGGGGATCATTTGCATCGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gggacaccttaggacacattctgtggagaagccgtacaagtgtgagttctgcggaagaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       687 CATGGGCCTTCCGGGCACAGTGTACCCAGTCATTAAAGAAGAAGTAAGCACAGTGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtgcggggcatctttactcagaaaggtaacctcctccgtcatattaaactgcacacggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567 TGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATGTGGGATATTGTGGCCGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccctgacct - - gggggacgctgcaagtgtggaggcaagacacatcaaagc - - - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 411.8; DB 1; Length 1551;
Pred. No. 5.5e-94;
0; Mismatches 387; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity 63.3
777; Conservative
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Best Local S
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                                                                                                                                                                            1053 CAGCGGTCTTATCTACCTGACCACCACCCGCCCGACGCGCAACGCGTGTCG---- 1108
                                                                                                                                                                                                                     tettetgaaggaggteettegetetttgaacteeteaageeeetteeatetgeetgag 1674
                                                                                                                                                                                                                                                           ----CTCAAGGAGGAGCACCGCGCCTACGACCTGCTGCGCGCCGCCTCCGAGAACTCGCA 1163
                                                                                                                                                                                                                                                                                                                                   GGACGCGCTCCGCGTCAGCACCAGCGGGGAGCAGATGAAGGTGTACAAGTGCGAACA 1223
                                                                                                                                                                                                                                                                                                                                                                             ctgccacgtcctcttcctagattatgtgatgttcaccatccacatggggtgccatggttt 1794
                                                                                                                                                                                                                                                                                                                                                                                               CGCCGTGGAGTACCTGCTGCTGCTCTCCAAGGCCAAGTTGGTGCTGCCCTCGGAGCGCGAGGC 992
                                                              gtccccaataacagtgcccaggactccacagacaccgacagcaaccacgaggatc----
                                                                                  ccgtgatccctttgagtgtaacatgtgtggctatcgaagccacgatcgctatgagttctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-2AN-1999 (first entry)
Human Ikaros isoform hlk-1 cDNA.
Haros hlk-1: transcription factor; human; lymphocyte;
cell differentiation; T cell; cancer; mmunodeficiency;
Alzheimer's disease; therapy; diagnosis; ss
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/*tag- a

/*number- Ex1

27 . .163

/*tag- b

/*tag- Ex2

164 . 420
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715. .849
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05-SEP-1996; US-711417.
(GEHO ) GEN HOSPITAL CORP.
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P-PSDB; W7097;
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This is the nucleotide of human Ikaros CDNA (isoform hIk-1) that codes for a 461-amino acid zinc finger protein (see W70964) that is involved in the early differentiation of lymphocytes. It was isolated from a Jurkat T cell line library using mouse Ikaros exon 7 cDNA as probe. The Ikaros gene maps between pll.2-pl3 on human and wuchnonsome 7. The human and murine Ikaros sequences (see 442805-11 and V42840) are highly conserved. Differential splicing of Ikaros
                        --gccaacatctctaccagcaaagccacgtggtcctcccccaggcccgcaatgggatgcc
                                          ctgccacgtcctcttcctagattatgtgatgttcaccatccacatggggtgccatggttt
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                                                                                                                                                                                                                                                  ccgtgatccctttgagtgtaacatgtgtggctatcgaagccacgatcgctatgagttctc
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                                                                               tettetgaaggaggteettegetetttgaacteetcaageeeeeteegag
                                                                                                                                       Human Ikaros isoform hik'ī cDNA.
Ikaros; hIK-1; transcription factor; human; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; ss.
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/number= Ex6
685. .1386
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550. .684
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/number= Ex7
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/*tag= b
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02-JAN-1997; 194256.
05-SEP-1996; US-711417.
(GEHO ) GEN HOSPITAL CORP.
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WPI; 98-378292/33.
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gene transcripts gives rise to different Ikaros protein isoforms.

If a invention provides Ikaros nucleic acids, vectors and host cells expressing Ikaros proteins. These are used to treat T and B cell diseases (e.g. immune deficiencies caused by drugs, radiation or cancers), to control expression of heterologous genes placed under control of an Ikaros-responsive element, to treat nervous system diseases (e.g. Alzheimer's disease) and to modulate cell division, emplification or differentiation, especially in haematopoietic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences. The same effect can be achieved with Ikaros-binding oligonocleotides. Examining the expression of the Ikaros gene, or its allelic structure, can be used to assess risk of acquiring the above diseases.

Sequence 1386 BP; 352 A; 403 C; 397 G; 234 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1441 ggagatggaaaagaaacggatcctcctgccagagaagatcttgccttctgaacgaggtct 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 TGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATGTGGATATTGTGGCCGAAG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 CTATAAACAGCGAACGTCTTTAGAGGAACATAAAGAGCGCTGCCACAACTACTTGGAAAG 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     873 GTACCAGCTGCACAGGCGCTCGGAGGGCACCCGCGCTCCAACCACTCGGCCCAGGACAG 932
                                                                                                                                                                                                                                                                                                                                                                                                     162 CATTCGACTTCCTAACGGAAAACTAAAGTGTGATATCTGTGGGATCATTTGCATCGGGCC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cttcgatgccaactacaatcccggctacatgtacgagaaggagaacgagatgatgcagac
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                                                                                                                                                                                                                                                                                          Score 411.8; DB 1; Length 1386;
Pred. No. 5.3e-94;
); Mismatches 387; Indels 63;
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Disclosure; Column 55-58; 111pp; English.

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFKB element or an itaros binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFKB element or an itaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring itaros isoform to any of a delta A element, an NFKB element or an itaros binding oligonucleotide consensus sequence; (d) it competitively inhibits faros binding oligonucleotide consensus sequence; (d) it competitively inhibits protein interactions of transcriptional complexes of the inhibits protein protein interactions of transcriptional complexes formed with naturally occurring itaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFKB elements and/or itaros-binding oligonucleotides, bind to delta A elements, NFKB elements and/or itaros-binding oligonucleotides,
                                                                                                                                                                                                                                                                                             --gccaacatctctaccagcaaagccacgtggtcctcccccaggcccgcaatgggatgcc 1614
                                                                                                                                                                                                               GGACGCGCTCCGCGTGGTCAGCACCAGCGGGAGCAGATGAAGGTGTACAAGTGCGAACA 1223
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CGCCGTGGAGTACCTGCTGCTCTCCAAGGCCCAAGTTGGTGCCCTCGGAGCGCGCAGGC 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-1999 (first entry)
Human Ikaros encoding cDNA.
CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS;
                                                                                                                                  tcttctgaaggaggtccctcgctctttgaactcctcaagccccctcccatctgcctgag
                                                                                                                                                            ----CTCAAGGAGGAGCACCGCGCCTACGACCTGCTGCGCGCCGCCTCCGAGAACTCGCA
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14-SEP-1992; US-946233.
14-SEP-1993; US-121438.
05-JUN-1995; US-465590.
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20-OCT-1998.
05-JUN-1995; 465590.
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competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements. NFKB elements and/or Ikaros binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros responsive elements and/or inhibit protein-protein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence encodes a specifically claimed human Ikaros protein.
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llarity 63.3%; Pred. No. 5.3e-94;
Conservative 0; Mismatches 387;
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Best Loca
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                                                                                                                                Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders
                                                               tcttctgaaggaggtccctcgctctttgaactcctcaagcccctcccatctgcctgag
                                                                                                                                                      GGACGCGTTCCGCGTGGTCAGCACCAGCGGGGGGGAGCAGATGAAGGTGTACAAGTGCGAACA
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                        ggagatggaaaagaaacggatcctcctgccagagaagatcttgccttctgaacgaggtct
                                      CGCCGTGGAGTACCTGCTGCTGCTCCCAAGCCCAAGTTGGTGCCCTCGGAGCGCGAGGC
                                                                                                gtcccccaataacagtgcccaggactccacagacaccgacagcaaccacgaggatc----
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immunocomprised; immune system disorder; nervous system disorder;
animal model; ss.
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29-JUL-1994; US-283300
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P-PSDB; R92015
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Disclosure; Fig 2; 102pp; English.

An almost full-length CDNA sequence (T16060) codes for part (R92015) of the human Ixaros protein, a master regulator of haematopoietic differentiation. It was isolated from a T-cell line Jurkat CDNA library using a mouse Ixaros CDNA clone as probe. The human Ixaros gene maps to pll.2-pll3 on chromosome 7.

Different isoforms (see R92014 and R92016-19) of mouse Ixaros have also been isolated. Transgenic animals, pref. mice, having a mutated Ixaros transgene, esp. a mutation that allers the DNA binding domain of the Ixaros protein, are used as models to determine the effects of treatments for immune or nervous system
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                                                                                                                                                                                                                                                                                                                                  395 G;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 411.8; DB 1;
Pred. No. 5.3e-94;
0; Mismatches 387;
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                                             Georgopoulos K;
WPI; 94-118387/14.
P-PSDB; R46964.
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                                                                                                          Gaps
                                                                                                                                committed lymphoid progenitors and in T and B cells, and is a transcriptional activator of a lymphoid gene. Aiolos cDNA can be used to produce recombinant Aiolos polypeptide (W15575) in host cells. The Aiolos polypeptide, coding sequence or cells expressing Aiolos may be used to treat a disorder in an animal, esp. by gene therapy. Such disorders include T-cell leuksemias and lymphomas. Non-wildtype gene structure or expression is indicative of a risk for such a disorder. Transgenic animals with an Aiolos transgene
                                                                                                                                                                                                                                                                          disorder; therapy; treatment;
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25.0%;
Best Local Similarity 88.1%;
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a
                                                                                                                                                                                                                                                                           be used in
                                                                                                                                                                                                  T-cell pathway regulatory gene, Ikaros - encodés family of unique zinc finger proteins, useful for treating immune system disorders claim 13; Page 44-46; 112pp; English.

The Ikaros gene encodes a zinc finger protein which can be used in therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is risk for an immune disorder. It is of particular use in treating disorder of the corpus striatum.

Sequence 1611 BP; 375 A; 484 C; 480 G; 272 T;
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63.1%; Pred. No. 1.8e-94;
ive 0; Mismatches 397;
with Ikaros
/product= Peptide
                                                                                      14-SEP-1992; US-946233.
(GEHO ) GEN HOSPITAL CORP
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Partial human Aiolos CDNA (T60491) was isolated by PCR amplification using primers (see also T60494-95) based on mouse Aiolos gene expression is restricted to lymphoid inneage. Aiolos polypeptide can form dimers with Aiolos or Ikaros polypeptides, is expressed in
ggagatggaaaagaaacggatcctcctgccagaagatcttgccttctgaacgaggtct
                                            gtococcaataacagtgcccaggactccacagacaccgacagcaaccacgaggatcgcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Aiolos partial CDNA.
Aiolos; transcription activator; immune system; T lymphocyte; B lymphocyte; Leukaemia; lymphoma; asthma; gene therapy; transgenic animal; ss.
Homo sapiens.
W09714714-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-1997.
17-OCT-1996; U16774.
18-OCT-1995; US-005529.
14-MAX-1996; US-017646.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                             T60491 standard; cDNA; 628
T60491;
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WPI; 97-245047/22.
P-PSDB; W15575.
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Compugen Ltd. GenCore version Copyright (c) 1993 - 1998

sw model using nucleic search, OM nucleic

November 5, 1999, 21:32:29 ; Search time 70:34 Seconds (without alignments) 7056.882 Million cell updates/sec .. 0 Run

US-09-019-348-1 1984 1 cacgagcgcacaccgctcgg......gaactcaaacccacctcgag 1984 Perfect score: Title:

Sequence:

IDENTITY_NUC Scoring table:

Searched:

311585 seqs, 125096042 residues

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	se Aiolos	Human Aiolos parti	ß	ß		·		Murine Ikaros cDNA	9	E Ikaros i	Ikaros i	ine Ikaros	e Ikaros		Ikaros cDNA. Trans	Ikaros isoform enc	m	Mouse Ikaros isofo	e Ikaros	Mouse Ikaros encod	s protein	Ikaros	e Ikaro	s protei	Ikaros	Ikaros e	Ikaros i	Ikaros is	s protein	os proteir		-ZBP	an SRE-ZBP	clone AW9	10	encoding an a	inger	-binding zinc-	finger prot	gene si	OTK18	Human OTK18 gene.
SUMMARIES	ID	6049	6049	044980	1606	969	V42806	284	909	697	280	280	497	605	969	909	697	281	280	T16063	697	712	909	909	711	V66973	697	280	V42810	712	712	996	348	348	658	363	946	697	457	857	537	V01890	V01891
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	Length	1984	62	61	38	38	38	55	9	9	9	78	78	78	78	8	8	8	17	1170	17	71	g	12	20	2	29	29	12	9	16	9	68	16	2	9	ø	26	æ	47	32	m	75
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EST clone Co1069.

V89789

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TRP-1 protein codi
Genetic locus bcl-
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Disclosure; Page 73-76. Hispp: English.

A cDNA clone (T6040) corresponds to the mouse Aiolos gene, a homologue of Ikaros whose expression is restricted to lymphoid commonly that spanned nucleotides 796-1156 of the sequence. Inneage. Aiolos CDNA was isolated from a mouse spleen CDNA library using a probe that spanned nucleotides 796-1156 of the sequence. Aiolos (W15574) can form dimers with Aiolos or Ikaros polypeptides, as expressed in committed lymphoid progenitors and in T and B cells, and is a transcriptional activator of a lymphoid gene. Primers of see also T6049-95) based on mouse Aiolos gene exons were used to amplify a human partial Aiolos CDNA (see also T60491). Aiolos CDNA can be used to produce recombinant Aiolos in transformed host cells. The Aiolos polypeptide, coding sequence or cells expressing Aiolos may be used to treat a disorder in an animal, esp. by gene therapy. Such disorders include T-cell lenkramias and lymphomas. Transgenic animals are provided with an Aiolos transgenic Sequence 1984 BP; 512 A; 570 C; 535 G; 357 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aiolos polypeptide and corresponding DNA - used to reconstitute a mammalian immune system, for the treatment of T cell leukaemia(s)
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                                                                                                                                                                                       Mouse Aiolos CDNA.
Aiolos, transcription activator; immune system; T lymphocyte;
B lymphocyte; leukaemia; lymphoma; asthma; gene therapy;
transgenic animal; ss.
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99.9%; Pred. No. 0;
Live 0; Mismatches
                                                               ALIGNMENTS
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374. 1897
/*tag= a
 T42903
Q80513
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                                                                                                                                        T60490 standard; cDNA; 1984 T60490;
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18-OCT-1995; US-005529.
14-MAY-1996; US-017646.
(GEHO ) GEN HOSPITAL CORP.
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Best Local Similarity 99.9 Matches 1982; Conservative
 3776
3720
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WPI; 97-245047/22.
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AVIERLASNWGKRKSSTPQRFLGEKLMRYGYPDLHEDMAYEREAEIIQSQMUDQAINN
ATYLGADALLPHISAAMPEVPIVSSLYSQYYHPARVERPTSRETSDSNDNNMD
GPISLIRPKNHRQPERASPSNSCLDTTDSESSHEAPALIPGHHANSRKQSSYYPKE
HGKPLDATKSSLGSSKDVYRVFNSEGEQIRAFKCEHCRVLFLDHVMYIHMG"
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Pred: No. 2.1e-23;
0; Mismatches 394; Indels 75
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                                                                                                                                     7.4%;
illarity 52.0%;
Conservative 0
                                                                                                                                                      Similarity
                                                                            295
                                                                                                                                                     Best Local Sim
Matches 508;
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Search completed: November Job time: 4688 sec

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Xenopus laevis
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SPEGGPGELMQPHVIDQAINSINTALAESCHSPTSSTSSDMGVMGSMFITGERKFSNI
SFEGGPGELMQPHVIDQAINSINTALAESCHPRIQTSPTSSDMGVMGSMFPHRPPA
EGHGLSAKDSAARALLLLAKKSASSEKOGSPSHSGQDSTDFESNNEEKAGVGASGLI
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RILFLDHVMYTIHMGCHGFRDPFECNLCGHRSQDRYEFSSHMTRGEHRY"
                                                                                                                                                                      /note="IX-8 isoform; similar to mouse and human larcs/LyF-1; alternatively spliced form missing exons and 6"
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y, Grenzacherstrasse 487, Basel CH-4005, Switzerland
Gocation/Qualifiers
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                                                               /strain="shasta"
/db_xref="taxon:8022"
/cell_type="thymocyte"
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Bi-Potential Primitive-Definitive Hematopoietic Progenitors in the
Vertebrate Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF024439 986 bp mRNA VRT 20-OCT-1997
Xenopus laevis ikaros-related transcription factor mRNA, partial
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Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae,
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1394 taccccatagcacttactcgggccgatatgccaatgggggccccgcaggagatggaaaag 1453
                                                   717 CTCCACAAGCCCCCTGCAGAGGCCCACGGCCTGTCAGCCAAGGACAGCGCGGAAAAT 776
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2 (bases 1 to 986)

Turpen,J., Kelley,C., Mead,P. and Zon,L.

Direct Submission
Submitted (10-Ssion
Longwood Ave, Boston, MA 02115, USA
Longwood Ave, Botton, MA 02115, USA
Longwood Ave, Botton,Qualifiers
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/db_xref="taxon:8355"
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/protein_id="AAB81280.1"
/db_xref="PID:92547232"
/db_xref="GI:2547232"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=3
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/codon_start=1
/product="rkaros homolog"
/product="rkaros homolog"
/protein_id="AaB53435.1"
/db_xref="rlb:2062744"
/db_xref="cl:2062744"
/db_xref="cl:2062744"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Protacanthopterygil;
Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 2079)
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                                                                       human Ikaros/LyF-1; composed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         974 tacaagtgigagttctgcggaagaagctacaagcagagaagctccctggaggagcacaag 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1034 gaacgctgccgagcttttcttcagaaccctgacctgggggacgctgcaagtgtggaggca 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
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Oncorhynchus mykiss Ikaros homolog (Ikaros) mRNA, Ik-8 isoform,
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       854 ctccgtcatattaaactgcacacgggggaaaaaccttttaagtgtcacctctgcaactac 913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGTGAACGGCCTTTCCAGTGCAACCAGTGTGGTGCCTCCTTTACCCAGAAGGGCAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GAGAGATGTCACAACTACCTACAAAGTATAGGCTTGCAGGGCCATCTTTATGCTGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GAAGAGGAAAATTGATATGGCAGAAGACCTGTCCAAGATTGGGTCAGAGATCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    794 ggcgaacgcccgttccagtgtaatcagtgcgggcatcttttactcagaaaggtaacctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submitted (06-MAR-1997) Comparative Immunol., Basel Inst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 166.2; DB 4; Length
Pred. No. 7.7e-28;
0; Mismatches 123; Indels
                                                                       mouse and
6"
                                            /gene="Ikaros"
/note="similar to
of exons 4, 5 and
/qene="Ikaros"
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 65.3%;
Matches 271; Conservative
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Hansen, J.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XLU92202 415 bp mRNA VRT 02-MAY-1997
Xenopus laevis/gilii Ikaros homolog (Ikaros) mRNA, partial cds.
U92202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000 ctacaagcagagaagctcctggaggagcacaaggaacgctgccgagctttcttcagaa 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 cagcagaccaaccagtgggaagatgaactgcgacgtgtgcgggttatcctgcattagctt 759
                                                                                                                                                                                                                                                                            880 ggaaaaacttttaagtgtcacctctgcaactacgcatgccaaaggagagatgcgctcac 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 CGGCCACCTGAGGACGCACTCCGTTAGTTTTTGTTGTGGATATTGTGGCGGAG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465 CTATAAACAGCGAAGCTCTTTAGAGGAGCATAAAGAGCGATGCCACAACTACTTGGAAAG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525 CATGGGCCTTCCGGGCATGTACCCAGTCATTAAGGAAGAAACTAACCACAACGAGGATGGC 584
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Submitted (06-MAR-1997) Comparative Immunol., Basel Inst. for
Immunology, Grenzacherstrasse 487, Basel CH-4005, Switzerland
Location/Qualifiers
                                                                                                                                                                                                                                               760 caacgictigaiggilcataagcgaagccaiaccggcgaacgcccgilccagigiaaica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       940 gggacaccttaggacacattctgtggagaagccgtacaagtgtgagttctgcggaagaag
                                                                                                                                                                                                                                                                                                                                                      820 gigogogoalcititacicagaaaggiaaccicciccgicatatiaaacigcacacggg
                                                                                              27;
                                          Length 684;
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Xenopus laevis/gilli
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                              Indels
                                            DB 12;
                                       Score 187.2; DB 12;
Pred. No. 1.5e-32;
); Mismatches 153;
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/db_xref="taxon:8359"
/dsue_type="thymus"
/clone_lib="LG15.0"
<1. >415
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                                       9.4%;
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U92202.1 GI:2062743
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2 (bases 1 to 415)
Hansen,J.D.
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                                                                    Best Local Similarity 65.1
Matches 336; Conservative
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ORIGIN
INYLGAESLRPLIQTSPTSSDMGVMGSMYPLHKPPAEGHGLSAKDSAAENLLLLAKSK
SASSEKDGSPSHSGODSTDTESNDEERAGVGASGLIYLTNHTISGVRNGVLPIVKEED
SROYEAMRASIEIASGEFKVLSGEGERVRAYRCEHCRILFLDHVMYTIHMGCHGFRDP
FRCNLCGHRSQDRYEESSHWIRGEHRY" 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcatcggtgagaagcggcactgcttcgatgccaactacaatcccggctacatgtacgaga 1250
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                                                                                                                                                                                                                                                                                                       576
                                                                                                                                                                 ccagtgggaagatgaactgcgacgtgtgcgggttatcctgcattagcttcaacgtcttga 770
                                                                                                                                          Gaps
                                                                                                                                                                                                                     tggttcataagcgaagccataccggcgaacgcccgttccagtgtaatcagtgcggggcat
                                                                                                                                                                                                                                      ctttactcagaaaggtaacctcctccgtcatattaaactgcacacgggggaaaacctt
                                                                                                                                                                                                                                                                                         CITICACCCAGAAAGGCAACCIGCIACGTCAAGCICCACCAGAGAAGACCT
                                                                                                                                                                                                                                                                                                                                 ttaagtgtcacctctgcaactacgcatgccaaaggagagatgcgctcacgggacacctta
                                                                                                                                                                                                                                                                                                                                                                                                      1251 aggagaacgagatgatgcagacccggatgatggaccaagccatcaataacgccatcagct
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                                                                                                                                                                                                                                                                                                                                                                                      ggacacattctgtggagaagccgtacaagtgtgagttctgcggaagaagctacaagcaga
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                                                                                                                                        Indels 147;
                                                                                                            Length 2301;
                                                                                                          Score 208.6; DB 4;
Pred. No. 2.4e-37;
0; Mismatches 404;
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                                                                                                          10.5%;
illarity 53.7%;
Conservative
                                                                                                                       Best Local Similarity
Matches 638; Conserv
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Best Local 8
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CTAINSTALL OF "MDVOEGQDMSQVSGKESPPVSDTPDEGDEPMPVPEDLSTTSGAO ONSKSDRGMSWYKVETQSDEBNGRACEMURECCAEDLRMLDASGEKNNGSHRDQGSSA LISGVGGITRDPNGKLKCDICGIVCIGPWVLMVHKRSHTERFPCONGCGASFTOKGNLLR HIKLHSGEKPPRCHLCGIVCIGPWVLMVHRPHSVGKPHRGCYGGRSYKORSSLEEHK ERCHNYLESMGLPGMYPVIKETHNNEMAEDLCKIGAERSLVLDRLASNVAKRSSMP OKFLDKCLSDMPYDSANYEKEDMMTSHYMDQAINNAINYLGAESLRPLVQTPFGSSEV VPVISSMYCHKPPSGOFFSNNSAODANDLLLLSKAKSVSSEREASPSNSCOPSTD TESNAEDGNSGLITTHNIPHARNGTALKEEDRAYEVLRAASBNSCODSTD TESNAEDGNSTTERSETH
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isoform VI"
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Ikaros/LyF-1-lymphoid transcription factor LyF-1 isoform VI
falternatively spliced} [mice, RLmll, Tdt+ thymoma, mRNA Partial,
574708
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Tobases 1 to 684)
Hahm, K., Ernst, P., Lo, K., Kim, G.S., Turck, C. and Smale, S.T.
Hahm, K., Ernst, P., Lo, K., Kim, G.S., Turck, C. and Smale, S.T.
The lymphoid transcription factor LyF-1 is encoded by specific, alternatively spliced mRNAs derived from the Ikaros gene Mol. Cell. Biol. 14 (11), 7111-7123 (1994)
95021239
GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 158967) from the original journal article. This sequence comes from Fig. 7A.
Location/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                            1291 AGGIGAGGCATATCGCTGTGAACACTGCCGCATCCTCTTCCTAGACCATGTGTACA
                                                                                                                1231 TGCGGGCCAGTATCGAGATTGCCTCGGAGGGGTTCAAGGTGCTGAGTGGAGAGGGGGAGC
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/portein_id="Ana32250.1"
/db_xref="PID:9807153"
/db_xref="GI:807153"
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/note="This sequence comes
/codon_start=1
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/db_xref="taxon:10095"
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/note="lymphoid trans
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Mus sp.
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/product="tkaros homolog"
/protein_id="aaB53432.1"
/protein_id="aaB53432.1"
/protein_id="pig2062736"
/db_xref="eii0562736"
/translation="memeEaQEmSQMPGRDSPPPNDLSEENDEAMPIPEDLSASSNLQ
HNNRGDKEGLACNIKYEARCDEENGLAIDMANNGEEEEEEACELIRVLASGARVNGSH
AGGPDSKGPYSAGGIRLPNGKLKCDICGIVCIGPNVLMYHRRSHTGERPFOCTOCGA
SFTOKGNLLRHIKAHSGERPFRACHCONYACRRRDALSGHLRTHSVGRRPHCAYCGRSY
KORSSLEEHKERCHNYLOCMGLONSIYTGEKRFSNISFEGGPGELMOPHVIDQAINSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
Salmoniformes; Salmonidae; Oncorhynchus.
I (bases 1 to 2301)
Hansen,J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolation and characterization of Ikaros homologues in the rainbow
                                                                                                                                                                                                                                                                                                                    tccacatggggtgccatggtttccgtgatccctttgagtgtaacatgtgtggctatcgaa 1832
   1936 CATCCCCCAGCAATGGCTGCCAGGACTCCACAGATACAGAGAGCAACCACGAAGACCGGA 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMU92198 2301 bp mRNA VRT 02-MAY-1997
Oncorhynchus mykiss Ikaros homolog (Ikaros) mRNA, Ik-7 isoform,
complete cds.
U92198
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Basel CH-4005, Switzerland
                                      -----tcgccaacatctctaccagcaaagccacgtggtcctcccc
                                                                                                                                          2056 TGGGCCGGCACAGTCCCGCCTATGCCAAAGAGGACCCCAAACCACAGGGGGGTTACTGC
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                                                                     1996 TIGGIGGGTIGGIATCCCTICCTCAGGGICCCCACCCCAACCTCCTCCCACCATAGIGG
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                                                                                                           caggocogoaatgggatgcctcttctgaaggaggtccctcgctcttt--gaactcctca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Tk-7 isoform; similar to mouse and human
Ikaros/LyF-1; alternatively spliced form missing
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                      Hansen, J.D.

Hansen, J.D.

Hansen, J.D.

Hansen, J.D.

Listed (06-MAR-1997) Comparative Immunol.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

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/organism="Oncorhynchus mykiss"
/db_xref="taxon:8022"
/db_xref="taxon:8022"
/db_1_type="thymocyte"
36. .1469

'--noe" Ikaros"
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36. .1469
/gene="Ikaros"
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2 (bases 1 to 2301)
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                         121;
 Length 2309;
                        Indels
 DB 4;
                         444;
           Pred. No. 4.7e-49;
0; Mismatches 444
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 Score 260.6;
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Best Local Similarity 56.0%;
Matches 718; Conservative
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okoya, S., Kawabata, I., Ikeda, H. and
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1430 CAGCGGCATTTTGAGGCTTTGCGAGCAGCAGGAATGGATTTGAGTATAGCGTCATCAGAA 1489
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Mus.
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                                                                                         1490 GGATTTAAGGTGCTGAGTGGAGATGGAGAAGTGAGGGGGGGTACCGCTGTATCCACTGC
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Tojo,M., Takeda,J., Tanno,Y., Yokoya,S., Kawabata,I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
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Eos protein.
Mus musculus (strain:ICR) Newborn cDNA to mRNA.
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/protein_id="RAA36213.1"

/db_xref="PID:41037199"

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/db_xref="GI:4062983"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 2309)
Amemiya.C. and Kawasaki,H.
Characterization of zebrafish ikaros, a gene necessary for differentiation of the immune system
Unpublished
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715 Albany Street, Boston, MA 02118,
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Danio rerio ikaros mRNA, complete cds.
AF092175
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Amendya,C. and Kawasaki,H.
Direct Submission
Submitted (15-SEP-1998) Center fo
University School of Medicine, 71
USA
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/db_xref="taxon:7955"
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NLLLLARISKSASSENGSPSHGSQDSTDTESNNEEKAGYGASGLIYLNHITGGVRG
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                                                                                                                                                                                                                                          gaaaaaccttttaagtgtcacctctgcaactacgcatgccaaaggagagatgcgctcacg
                                                                                                                                                                                                                                                                                    670 GAGAAGCCCTTCAAATGTCCTTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCACA
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                                                                                                                                 DB 12; Length 1847;
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                                                                                                                                16.7%; Score 331.4; DB 12; 58.0%; Pred. No. 5.2e-65; iive 0; Mismatches 446;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
Salmoniformes; Salmonidae; Oncorhynchus.
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Ikaros/LyF-1; alternatively spliced form missing exon 3"
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                                                                                                                                                                                                                                                                                                                                                                               cacging tectececcagg cocgea transpart gettettet gaaggagg teet content 1639
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Oncorhynchus mykiss Ikaros homolog (Ikaros) mRNA, Ik-2 isoform,
complete cds.
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Submitted (OG-MAR-1997) Comparative Immunol., Basel Inst. for Immunology, Grenzacherstrasse 487, Basel CH-4005, Switzerland Location/Qualifiers
1. 2183
/organia=*Oncorhynchus mykiss"
/strain="shasta"
                                                                                                                                                                                        CTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCGC---CAGTCCTACCAAGGAAAC
                                                                     atcetectgecagagaagatettgeettetgaacgaggtetgteeceeaataacagtgee
                                                                                                              1330 TCTCTCATCAGACCAAAGAGTCGACCCAGGAAGAGAGGCCTCGCCCAGCAATAGCTGC
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50. .1336
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Isolation and characterization
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2 (bases 1 to 2183)
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/codon_start=1

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ISTNGWKLEMGSDEECROPLGSEDEIRGHIDEGSSLEEPLIESEVADNRKVODLQGE
GGIRLPNGKLKCDVCGMVCIGPNVLMVHKRSHTGERPFHCNQCGASFTQKGNLLRHIK
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Mus musculus multi-zinc finger protein helios mRNA, complete cds.
AF044257
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Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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   ccettagtecagaetecgeetgeteceaeetetgagatggteeeagteateageagtgtg 1393
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                                       1394 taccccatagcacttactcgggccgatatgccaatgggggccccgcaggagatggaaaag
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/product="multi-zinc finger
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/db_xref="taxon:10090"
178. .1758
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KQRSSLEEHKERCHNYLQCMGLQNSIYTVVKEESNQNBQREDLSQMGSKRALVLDRLA
NNVAKRKSTPPOKFVGEKRFSNISFEGGPGELMOPHVLDQALNSAINYLGAESLFRLI
OTSPTSSDMGVMGSMYPLHKPPRISFEGGLSAKDSAABLLLLLAKSKSASSERDGSPSHS
GQDSTDTESNNERKAWGASGLIYLTHNITSGYRNGYLPLVKEBQQRQYEAMASIEI
ASEGFKVLSGEGEQVRAYRCEHCRILFLDHVWYTIHMGCHGFRDPFECNLCGHRSQDR
                                                                                                                                                                                                                                /product-"ikaros homolog"
/product-"ikaros homolog"
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/db_xref="clb_g062742."
/db_xref-"dl:2062742."
/db_xref-"dl:
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                                                                                                                            /note="Ik-1 isoform; similar to mouse and human
Ikaros/LyF-1; Ikaros/LyF-1 homolog"
/codon_start=1
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/gene="Ikaros"
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/gene="Ikaros"
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QNSKSDRGMGERPFOCNQCGASFTOKGNILRHIKLHSGERPFKCHLCNYACRRRDALF
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GHLFTHSVGKFPKGGYCGRSYKORSSLEHKRENNTILESMGLPGVCPYKEETNHNE
MAEDLCKIGARRSLVLDRLASWARRKSSMPGKFLGARYCKLSDMYDFSDAYEREDMMYS
HVMDQAINNAINYLGABSLRPLVQTPPGSSEVVPVISSMYQLHKPPSDGPPRSNHSAQ
DAVDMILLLSKAKSVSSEREASPSNSCODSTDTESNAEEQRSGILYLTNHINPHARNG
HACKHGFRDPFECNAESHSQDAFRVYSTSGEQLKVYKCEHCRYLFLDHVMYTIHMGC
HGCHGFRDPFECNAESHSPRSCHAFFSSHITRGEHRYHLS"
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                                                                                                                                                                                                                                                                                                                                                        Score 348; DB 12;
Pred. No. 9.5e-69;
0; Mismatches 375;
                                                                                                                                                        /product="Ikaros DNA binding
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/db_xref="G1:198287"
                                                                                    EL4"
                          1. .1550
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/db_xref="taxon:10090"
                                                                               /tissue_lib="Lambda ZAP 39. .1334
                                                         /cell_type="T cell"
/dev_stage="adult"
            Location/Qualifiers
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Ouncorpynchus mykiss

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases i to 2496)
Hansen, J.D., Strassburger, P. and Du Pasquier, L.
Conservation of a master hematopoletic switch gene during
vertebrate evolution: isolation and characterization of Ikaros from
teleost and amphibian species
Eur. J. Immunol. 27 (11), 3049-3058 (1997)
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Oncorhynchus mykiss Ikaros homolog (Ikaros) mRNA, Ik-1 isoform,
complete cds.
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caggocogoaatgggatgcotcttctgaaggaggtcootcgcttttgaactootcaag
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PWGSEVVPVISPWOLHKPLGDNOTRSNHTAQDSAVENLLLISKAKSYSSERDASPSN
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Direct Submission
Submitted (12-MAR-1997) J.P. Lilppo, Turku Immunology Centre &
Department of Medical Microbiology, Turku University,
Kiinamyllynkatu 13, FIN-20520 Turku, FINLAND
Location/Qualifiers
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/organism="Reli"
/db_xref="taxon:9031"
/germline
/tissue_type="thymus"
/cell_type="T lymphocyte"
/clone_lib="pcDM8 thymus cDNA"
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DNA-bliding transcription factor; Ikaros; Ikaros DNA binding
protein; transcription; zinc finger protein; zinc-finger
transcription factor.
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HKERCHNYLESMGLPGTIFTPVIKEETRHSEMAEDLCKIGSERSLYLDRLASNVARKKS
SMPQKFLGDKGLSDTPYDSATYEKENEMAKSHVADQAINNAINYLGAESLRPLVQTPP
GGSEVVPVISPMYOLHRRSEGTPRSHHSAODSAVEYLLLLSKAKLVPGEREASPSNSC
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TSGEDMKVYKCEHCRVLFLDHVMYTIHMGCHGFRDPFECNMCGYHSQDRYEFSSHITR
GEHRFHMS"
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The Ikaros gene encodes a family of lymphocyte-restricted zinc finger DNA binding proteins, highly conserved in human and mouse L J. Immunol. 156 (2), 585-592 (1996)

E 96132984 in the National Library of Medicine created this GenBank staff at the National Library of Medicine created this entry [NOBI gibbsq 175401] from the Original journal article. This sequence comes from Fig. 1B and C. This sequence to This Palla Palla.

This Palla Palla Palla C. This Appla Palla Palla C. This Balla Palla Palla C. This Balla Palla                               human and mouse
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                                                                                                                                                                                                                                                                                                                     /note="hIK1"
238. 1788
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/gene="IKAROS"
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 1557)
                                                                                                                                                       1044 TAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGGCCCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtcccccaataacagtgcccaggactccacagacaccgacagcaaccacgaggatc----
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caatgtggctaagcgaaaaagctcgatgcctcagaaattcatcggtgagaagcggcactg
                                                                       cttcgatgccaactacaatcccggctacatgtacgagaaggagaacgagatgatgcagac
                                                                                              gtaccccata-----gcacttactcgggccgatatgccaatgggggcccgca
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Eur. J. Immunol. 27 (8), 1853-1857 (1997)
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Liippo, J.P.
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       GTACCAGCTGCACAAGCCGCTCGCGGAGGGCACCCCGCGCGTCCAACCACTCGGCCCAGGA 1268
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Homo sapiens
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/product="lkaros/LyF-1" homolog"
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                                                                                                                                     Direct Submission
Submitted (10-NOV-1995) Wilfried Nietfeld, Department of Virology,
University of Freiburg, Institute for Medical Microbiology and
Hygiene, Hermann-Herder-Strasse 11, Freiburg 79104, Germany
Location/Qualifiers
and sequencing of hIk-1, a cDNA encoding a human homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to mouse LyF-1, encoded by GenBank
Accession Number S74708; similar to mouse Ikaros
DNA-binding protein, Swiss-Prot Accession Number Q03267"
/codon_starte.
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Eutheria; Primates; Catarrhini; Hominidae;
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Nietfeld,W. and Meyerhans,A.
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd. OM nucleic - nucleic search, using sw mode! Run on: November 6, 1999, 05:21:26; Search time 701.47 Seconds (without alignments) 8995.016 Million cell updates/sec Title: US-09-019-348-1 Perfect score: 1984 Sequence: 1 cacgagagacacaccgctcgggaactcaaacccacctcgag 1984		25: em_oov:* 26: em_pot:* 28: em_pot:* 29: em_pl:* 29: em_pl:* 30: em_sts:* 31: em_sts:* 31: em_sts:* 32: em_uni:* 32: em_uni:* 33: em_uni:* 33: em_lni:* 34: gb_htg1:* 35: gb_htg2:* 36: gb_ln1:* 37: gb_ln1:* 38: em_ba1:* 39: em_ba1:* 39: em_ba1:* 39: em_lnm4:* 41: em_lnm4:* 42: gb_pr4:* SUMMARIES SCORE greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SCORE Match Length DB ID SCO